OM protein - protein search, using sw model
Run on: October 31, 2006, 02:26:34 ; Search time 199 Seconds
                                                    (without alignments)
                                                    537.631 Million cell updates/sec

Title:           US-10-063-518-14
Perfect score:   1195
Sequence:        1 MNHLPEDMENALTGSQSSHA.............EAGSEEAEEKQDSEKPLLEL 234
Scoring table:   BLOSUM62
Searched:        Gapop 10.0, Gapext 0.5
                 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
Database :       Listing first 1500 summaries
                 A_Geneseq_8.*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003aa:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

No.    Score  Match Length DB ID       Description
                                       SUMMARIES

RESULT 1
ID   AAU29056 standard; protein; 234 AA.
DE   Human PRO polypeptide sequence #33.
PN   WO20016848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.
Query Match        100.0%;  Score 1195; DB 4;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
(HYSE-) HYSEQ INC.

RESULT 2
ID   AAM39929 standard; protein; 234 AA.
DE   Human PRO polypeptide SEQ ID NO 3074.
PN   WO20015331Z-A1.
PD   26-JUL-2001.
PA   (GETH ) GENENTECH INC.
Query Match        100.0%;  Score 1195; DB 4;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 3
ID   AAB87532 standard; protein; 234 AA.
DE   Human PRO1864.
PN   WO20016318-A2.
PD   08-MAR-2001.
PA   (GETH ) GENENTECH INC.
Query Match        100.0%;  Score 1195; DB 4;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 4
ID   ABG95857 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein PRO1864.
PN   US200211930-A1.
PD   29-AUG-2002.
PA   (GETH ) GENENTECH INC.
Query Match        100.0%;  Score 1195; DB 5;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 5
ID   ABB84847 standard; protein; 234 AA.
DE   Human PRO1864 protein sequence SEQ ID NO:62.
PN   WO20020690-A2.
PD   03-JAN-2002.
PA   (GETH ) GENENTECH INC.
Query Match        100.0%;  Score 1195; DB 5;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 6
ID   ABB95453 standard; protein; 234 AA.
DE   Human angiogenesis related protein PRO1864 SEQ ID NO: 62.

PN   WO20020284-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
     (FERR/) FERRARA N.
     (GERB/) GERBER H.
     (GERR/) GERRITSEN M E.
     (GODD/) GODDARD A.
     (GODO/) GODOWSKI P J.
     (GURN/) GURNEY A L.
     (HILL/) HILLAN K J.
     (MARS/) MARSTERS S A.
     (PANJ/) PAN J.
     (PAON/) PAONI N F.
     (STEP/) STEPHAN J F.
     (WATA/) WATANABE C K.
     (WILL/) WILLIAMS P M.
     (WOOD/) WOOD W I.
Query Match        100.0%;  Score 1195; DB 5;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 7
ID   ABU58432 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US200302272-A1.
PD   06-FEB-2003.
Query Match        100.0%;  Score 1195; DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 8
ID   ABU87980 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200302127-A1.
PD   13-FEB-2003.
Query Match        100.0%;  Score 1195; DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 9
ID   ABU84295 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US200303112-A1.
PD   13-FEB-2003.
Query Match        100.0%;  Score 1195; DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 10
ID   ABR66169 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200302778-A1.
PD   06-FEB-2003.
Query Match        100.0%;  Score 1195; DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 11
ID   ABR65559 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200306159-A1.
PD   27-FEB-2003.
Query Match        100.0%;  Score 1195; DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 12
ID   ABU99499 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein #33.
PN   US200304070-A1.
PD   20-FEB-2003.
Query Match        100.0%;  Score 1195; DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 13
ID   ABU82738 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US200303113-A1.
PD   13-FEB-2003.
Query Match        100.0%;  Score 1195; DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 14
ID   ABU89859 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200306147-A1.

PD   20-FEB-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 15
ID   ABR68108 standard; protein; 234 AA.
DE   Novel human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027264-A1.
PD   06-FEB-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 16
ID   ABU96161 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036144-A1.
PD   20-FEB-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 17
ID   ABU92592 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003035149-A1.
PD   20-FEB-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 18
ID   ABU08669 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044923-A1.
PD   06-MAR-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 19
ID   AB002721 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040062-A1.
PD   27-FEB-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 20
ID   ABR74875 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040056-A1.
PD   27-FEB-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 21
ID   ABR94637 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044926-A1.
PD   06-MAR-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 22
ID   ABU85610 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003036140-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 23
ID   ABU98770 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003013153-A1.
PD   16-JAN-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 24
ID   ABU97985 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003017544-A1.
PD   23-JAN-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;

     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 25
ID   ABU91691 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003027277-A1.
PD   06-FEB-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 26
ID   ABU89384 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003036141-A1.
PD   20-FEB-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 27
ID   ABU86225 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036146-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 28
ID   ABU67438 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036162-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 29
ID   ABU80466 standard; protein; 234 AA.
DE   Human PRO protein #33.
PN   US2003036137-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 30
ID   ABU90882 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003018173-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 31
ID   ABO33941 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein PRO1864.
PN   US2003009013-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 32
ID   ABR99384 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040063-A1.
PD   27-FEB-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 33
ID   ABR98774 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040064-A1.
PD   27-FEB-2003.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 34
ID   ABO16297 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein 234 AA.
PN   US2003027267-A1.

PD   06-FEB-2003.
Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 35
ID   ABR92197 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030036160-A1.
PD   20-FEB-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 36
ID   ABO18838 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein; 234 AA.
PN   US20030044925-A1.
PD   06-MAR-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 37
ID   ABR78259 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054474-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 38.
ID   ABR39937 standard; protein; 234 AA.
DE   Human prostate selective polypeptide Pr340.
PN   WO200014298-A2.
PD   20-FEB-2003.
PA   (ORIG-) ORIGENE TECHNOLOGIES INC.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 39
ID   ABU71958 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030018183-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 40
ID   ABU84995 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030032114-A1.
PD   13-FEB-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 41
ID   ABO00134 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030032101-A1.
PD   13-FEB-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 42
ID   ABO11466 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO)
PN   US20030036124-A1.
PD   20-FEB-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 43
ID   ABO02111 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030040054-A1.
PD   27-FEB-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 44
ID   ABU88685 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030036133-A1.

PD   20-FEB-2003.
Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 45
ID   ABU83380 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036134-A1.
PD   20-FEB-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 46
ID   ABO06181 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030022294-A1.
PD   30-JAN-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 47
ID   ABR59217 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030027275-A1.
PD   06-FEB-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 48
ID   ABO09279 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030027324-A1.
PD   06-FEB-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 49
ID   ABO19143 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030036118-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 50
ID   ABO11161 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036123-A1.
PD   20-FEB-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 51
ID   ABR66779 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030036148-A1.
PD   20-FEB-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 52
ID   ABO15992 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030040060-A1.
PD   27-FEB-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 53
ID   ABO13698 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030044916-A1.
PD   06-MAR-2003.

Query Match     100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;
RESULT 54
ID   ABU71512 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864.
PN   US20030013855-A1.
PD   16-JAN-2003.
PA   (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 55
ID ABU65601 standard; protein; 234 AA.
DE Human secreted/transmembrane protein, SEQ ID 66.
PN US20030036156-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 56
ID ABO07449 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030032117-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 57
ID ABO03636 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030027266-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 58
ID ABR67084 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 59
ID ABU15687 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030222298-A1.
PD 30-JAN-2003.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 60
ID ABU55968 standard; protein; 234 AA.
DE Human secreted/transmembrane protein, PRO1864.
PN US20030222298-A1.
PD 30-JAN-2003.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 61
ID ABU72293 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US20020182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 62
ID ABU55296 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030032102-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 63
ID ABU95241 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030036117-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 64
ID ABU71144 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US20030036143-A1.
PD 20-FEB-2003.

Query Match

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 65
ID ABO07754 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030032130-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 66
ID ABR69995 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030032118-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 67
ID ABR69328 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030036132-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 68
ID ABO01469 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 69
ID ABU81271 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030017542-A1.
PD 23-JAN-2003.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 70
ID ABR60068 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030032137-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 71
ID ABR58287 standard; protein; 234 AA.
DE BCU0092 protein #SEQ ID 20.
PN WO200302942l-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 72
ID ABU90966 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 73
ID ABR67803 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030027269-A1.
PD 06-FEB-2003.

Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 74
ID ABR65191 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030027268-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 75
ID ABR68413 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027274-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 76
ID ABR71825 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 77
ID ABU85305 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022295-A1.
PD 30-JAN-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 78
ID ABU88995 standard; protein; 234 AA.
DE Human secreted/transmembrane protein #33.
PN US2003022297-A1.
PD 30-JAN-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 79
ID ABU83075 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032105-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 80
ID ABU94931 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032123-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 81
ID ABU90479 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032108-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 82
ID ABU83990 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032111-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 83
ID ABU93641 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032119-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 84
ID ABR64886 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 85
ID ABO27287 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO1864.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 86
ID ABR68718 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027271-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 87
ID ABO06534 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036125-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 88
ID ABR99079 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040068-A1.
PD 27-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 89
ID ABU56963 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027280-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 90
ID ABU85915 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022300-A1.
PD 30-JAN-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 91
ID ABU82202 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036136-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 92
ID ABU87213 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036138-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 93
ID ABU83685 standard; protein; 234 AA.
DE Human secreted/transmembrane protein #33.
PN US2003032109-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 94
ID ABO06059 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 95

ID   ABU92482 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein PRO1864.
PN   US200304584-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; DB 6; Length 234;

RESULT 96
ID   ABU81770 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200303104-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 97
ID   ABU65934 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200303157-A1.
PD   20-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 98
ID   ABU81152 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US200302212-A1.
PD   06-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 99
ID   ABR59763 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US200303120-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 100
ID   ABU33951 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200303155-A1.
PD   20-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 101
ID   ABU99804 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200303296-A1.
PD   30-JAN-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 102
ID   ABR66474 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US200302281-A1.
PD   06-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 103
ID   ABR90892 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US200302986-A1.
PD   06-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 104
ID   ABO53267 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200304058-A1.
PD   27-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Length 234;

RESULT 105
ID   ABU94319 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US200301754-A1.
PD   23-JAN-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; DB 6; Length 234;

RESULT 106
ID   ABU79201 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US200303129-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 107
ID   ABU86530 standard; protein; 234 AA.
DE   Novel human secreted/transmembrane protein (PRO) #33.
PN   US200303131-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 108
ID   ABU86835 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200303103-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 109
ID   ABU94624 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US200303107-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 110
ID   ABO04551 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 111
ID   ABR70300 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200303139-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 112
ID   ABU98465 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US200302301-A1.
PD   30-JAN-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Pred. No. 1.6e-131;

RESULT 113
ID   ABR65864 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200303165-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; Length 234;

RESULT 114
ID   ABR64581 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864.
PN   US200302262-A1.
PD   06-FEB-2003.
     Query Match
     Best Local Similarity 100.0%; 100.0%;   Score 1195; DB 6; Length 234;

RESULT 115
ID   ABU79506 standard; protein; 234 AA.
     Best Local Similarity

DE  Human PRO polypeptide #33.
PN  US2003032110-Al.
PD  13-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 116
ID  ABU89274 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003036142-Al.
PD  20-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 117
ID  ABU95856 standard; protein; 234 AA.
DE  Human PRO polypeptide #33.
PN  US2003036145-Al.
PD  20-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 118
ID  ABU91076 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein (PRO) #33.
PN  US2003036154-Al.
PD  20-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 119
ID  ABU90169 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003036153-Al.
PD  20-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 120
ID  ABU09584 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003044931-Al.
PD  06-MAR-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 121
ID  ABO10856 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003036150-Al.
PD  20-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 122
ID  ABR70910 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003040069-Al.
PD  27-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 123
ID  ABU98269 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2002183493-Al.
PD  05-DEC-2002.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 124
ID  ABU87518 standard; protein; 234 AA.
DE  Human PRO polypeptide #33.
PN  US2003022293-Al.
PD  30-JAN-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 125
ID  ABU91386 standard; protein; 234 AA.
DE  Human PRO polypeptide #33.
PN  US2003032128-Al.

PD  13-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 126
ID  ABU89274 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003036634-Al.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 127
ID  ABU84600 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003032116-Al.
PD  13-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 128
ID  ABR69690 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003032122-Al.
PD  13-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 129
ID  ABU80067 standard; protein; 234 AA.
DE  Human PRO protein #33.
PN  US2003036139-Al.
PD  20-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 130
ID  ABU82481 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2002183494-Al.
PD  05-DEC-2002.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 131
ID  ABU93336 standard; protein; 234 AA.
DE  Human PRO polypeptide #33.
PN  US2003017541-Al.
PD  23-JAN-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 132
ID  ABO09889 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003017543-Al.
PD  23-JAN-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 133
ID  ABO08974 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003036152-Al.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 134
ID  ABU96445 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003027993-Al.
PD  06-FEB-2003.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 135
ID  ABU10542 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein #33.
PN  US2002127584-Al.

PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
DE   Human PRO polypeptide #7.
ID   ABU72115 standard; protein; 234 AA.
PN   US20030023042-A1.
PD   30-JAN-2003.

RESULT 136
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PD   13-FEB-2003.
PN   US20030032115-A1.
DE   Human PRO polypeptide #33.
ID   ABU95551 standard; protein; 234 AA.
PA   (GETH ) GENENTECH INC.

RESULT 137
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PD   13-FEB-2003.
PN   US20030032140-A1.
DE   Novel human secreted and transmembrane protein PRO1864.
ID   ABU96760 standard; protein; 234 AA.

RESULT 138
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PA   (GETH ) GENENTECH INC.
PD   27-FEB-2003.
PN   US20030040076-A1.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
ID   ABR70605 standard; protein; 234 AA.

RESULT 139
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PA   (GETH ) GENENTECH INC.
PD   09-JAN-2003.
PN   US20030008352-A1.
DE   Novel human secreted and transmembrane protein PRO1864.
ID   ABO04956 standard; protein; 234 AA.

RESULT 140
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PD   06-MAR-2003.
PN   US20030044922-A1.
DE   Human secreted/transmembrane protein (PRO) #33.
ID   ABO08364 standard; protein; 234 AA.

RESULT 141
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PD   13-FEB-2003.
PN   US20030032118-A1.
DE   Human secreted/transmembrane protein (PRO) #33.
ID   ABO05571 standard; protein; 234 AA.

RESULT 142
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PD   20-FEB-2003.
PN   US20030036135-A1.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
ID   ABR73960 standard; protein; 234 AA.

RESULT 143
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PD   20-MAR-2003.
PN   US20030054455-A1.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
ID   ABR95552 standard; protein; 234 AA.

RESULT 144
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PA   (GETH ) GENENTECH INC.

RESULT 145
ID   ABR80849 standard; protein; 234 AA.

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DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049741-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
ID   ABR81154 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049743-A1.
PD   13-MAR-2003.

RESULT 146
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PA   (GETH ) GENENTECH INC.
PD   13-MAR-2003.
PN   US20030049769-A1.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
ID   ABM00850 standard; protein; 234 AA.

RESULT 147
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PA   (GETH ) GENENTECH INC.
PD   10-APR-2003.
PN   US20030068743-A1.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
ID   ABR88452 standard; protein; 234 AA.

RESULT 148
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PA   (GETH ) GENENTECH INC.
PD   20-MAR-2003.
PN   US20030054479-A1.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
ID   ABM77273 standard; protein; 234 AA.

RESULT 149
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PA   (GETH ) GENENTECH INC.
PD   10-APR-2003.
PN   US20030068685-A1.
DE   Human secreted/transmembrane protein (PRO) #33.
ID   ABO28757 standard; protein; 234 AA.

RESULT 150
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PA   (GETH ) GENENTECH INC.
PD   10-APR-2003.
PN   US20030068725-A1.
DE   Human secreted/transmembrane protein (PRO) #33.
ID   ABO31502 standard; protein; 234 AA.

RESULT 151
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PA   (GETH ) GENENTECH INC.
PD   10-APR-2003.
PN   US20030068752-A1.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
ID   ABM07919 standard; protein; 234 AA.

RESULT 152
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;
PA   (GETH ) GENENTECH INC.
PD   10-APR-2003.
PN   US20030068682-A1.
DE   Human secreted/transmembrane protein (PRO) #33.
ID   ABO40399 standard; protein; 234 AA.

RESULT 153
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
Query Match    100.0%;   Score 1195;   DB 6;   Length 234;

RESULT 154
ID   ABO35824 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.

PN  US20030687701-A1
PD  10-APR-2003
PA  (GETH ) GENENTECH INC.

RESULT 155
ID  ABO43963 standard; protein; 234 AA.
DE  Human PRO polypeptide #33; 234 AA.
PN  US20030687055-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 156
ID  ADA77818 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US20030731180-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 157
ID  ABM24758 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20031045339-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 158
ID  ABO03026 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US20030536131-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 159
ID  ABR90282 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20030040075-A1.
PD  27-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 160
ID  ABM17196 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20030054459-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 161
ID  ABR94942 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20030044930-A1.
PD  06-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 162
ID  ABR95247 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20030040071-A1.
PD  27-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 163
ID  ADB17071 standard; protein; 234 AA.
DE  Human transmembrane PRO polypeptide (SeqID 14).
PN  US20030050462-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 164
ID  ABO21485 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US20030054471-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 165
ID  ABR97749 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20030644452-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 166
ID  ABR87537 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20030687055-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 167
ID  ABM77578 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20030544473-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 168
ID  ABM27808 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20030644440-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 169
ID  ABM06089 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20030687704-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 170
ID  ABM03595 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20030687722-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 171
ID  ABM35046 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864; protein; 234 AA.
PN  US20030731183-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 172
ID  ABM26283 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US20031045549-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;
    Best Local Similarity  100.0%;    Score 1195;  DB 6;  Pred. No. 1.6e-131;  Length 234;

RESULT 173
ID  ABO48065 standard; protein; 234 AA.

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DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003049749-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 174
ID  ABP92807 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003064462-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 175
ID  ABO24568 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003065159-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 176
ID  ABM11579 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003064447-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 177
ID  ABM02680 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003073184-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 178
ID  ABM15976 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003064463-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 179
ID  ABO27537 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003064451-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 180
ID  ABM29028 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003068721-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 181
ID  ABM07004 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003068699-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 182
ID  ABM21098 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.


PN  US2003068707-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 183
ID  ABM09444 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003073175-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 184
ID  ABO41314 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003068695-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 185
ID  ABO36129 standard; protein; 234 AA.
DE  Human PRO polypeptide #33.
PN  US2003068703-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 186
ID  ABO43658 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003068732-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 187
ID  ABM76358 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003082717-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 188
ID  ABM76054 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003104548-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 189
ID  ABM25673 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003104542-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 190
ID  ABM25978 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003104543-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 191
ID  ABO03331 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003061127-A1.
PD  20-FEB-2003.
    Query Match             100.0%;  Score  1195;  DB 6;
    Best Local Similarity   100.0%;  Pred. No. 1.6e-131;  Length 234;
```

RESULT 192
ID   ABO02416 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040061-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;
                        100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 193
ID   ABO44245 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO 1864.
PN   US2003018172-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;
                        100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 194
ID   ABR90587 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036130-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;
                        100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 195
ID   ABR73655 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054468-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;
                        100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 196
ID   ABO16907 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054470-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;
                        100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 197
ID   ABR94332 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044917-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;
                        100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 198
ID   ABR75839 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044929-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;
                        100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 199
ID   ABR71215 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059880-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;
                        100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 200
ID   ABR93112 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064465-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;
                        100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 201
ID   ABR93417 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054478-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 202
ID   ABR87842 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068718-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 203
ID   ABO27842 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064454-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 204
ID   ABO29977 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064461-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 205
ID   ABO31186 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068724-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 206
ID   ABM04874 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068727-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 207
ID   ABM08834 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068772-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 208
ID   ABO36434 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068714-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 209
ID   ABO35519 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068758-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   100.0%;   Pred. No. 1.6e-131;
                        Score 1195;   DB 6;   Length 234;

RESULT 210
ID   ABO39484 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068776-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 211
ID   ABM10359 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030069407-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 212
ID   ABM11884 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104555-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 213
ID   ABO52030 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030049768-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 214
ID   ABO52335 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030049771-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 215
ID   ADA19876 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030069394-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 216
ID   ABO23653 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030032134-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 217
ID   ADB17259 standard; protein; 234 AA.
DE   Human transmembrane PRO polypeptide (SeqID 14).
PN   US20030050465-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 218
ID   ABR97139 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054481-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 219
ID   ABR86927 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049778-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 220
ID   ABM10969 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049782-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 221
ID   ABM28813 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054476-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 222
ID   ABO32112 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068733-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 223
ID   ABM15239 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068692-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 224
ID   ABM06394 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068709-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 225
ID   ABM04205 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068716-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 226
ID   ABM22318 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068751-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 227
ID   ABM07614 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068740-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 228
ID   ABO40704 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068684-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195;  DB 6;  Length 234;

RESULT 229
     Best Local Similarity

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ID   ABM35351 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073179-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 230
ID   ABM33114 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030087374-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 231
ID   ABO52640 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030049773-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 232
ID   ABO50200 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049777-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 233
ID   ABU09194 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030040055-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 234
ID   ABO04246 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036164-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 235
ID   ABO05876 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030040074-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 236
ID   ABM18416 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054480-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 237
ID   ABR97444 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030059885-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 238
ID   ABR80544 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049740-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 239
ID   ABM01155 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049770-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 240
ID   ABR88757 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073169-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 241
ID   ABM13409 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064457-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 242
ID   ABM20793 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068711-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 243
ID   ABO41924 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049745-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 244
ID   ABO42534 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049751-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 245
ID   ABM10054 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030067478-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 246
ID   ABO38569 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068773-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 247
ID   ABM32809 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073185-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
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RESULT 248
ID   ABM22623 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030087373-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 249
ID   ABM74834 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030096353-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 250
ID   ADA79610 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003071173-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 251
ID   ABR96224 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054458-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 252
ID   ABR86317 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049758-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 253
ID   ABM02375 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030059886-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 254
ID   ABR86622 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049772-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 255
ID   ABM16586 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064448-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 256
ID   ABM29638 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064456-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 257
ID   ABO29062 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068693-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 258
ID   ABM23843 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068735-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 259
ID   ABM23233 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068753-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 260
ID   ABM22013 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068742-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 261
ID   ABO37654 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068756-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 262
ID   ABM28418 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030082715-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 263
ID   ABM28723 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030082716-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 264
ID   ABM66367 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030082737-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 265
ID   ABM75749 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104547-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 266
ID   ABM34029 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030096359-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
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RESULT 267
ID   ABM34334 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20031000661-A1.
PD   29-MAY-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 268
ID   ABO20265 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030032125-A1.
PD   13-FEB-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 269
ID   ABO21180 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030054454-A1.
PD   20-MAR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 270
ID   ABO22095 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030054477-A1.
PD   20-MAR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 271
ID   ADA20048 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030055222-A1.
PD   20-MAR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 272
ID   ABO34173 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO 1864.
PN   US20030060601-A1.
PD   27-MAR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 273
ID   ABR96529 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864.
PN   US20030054460-A1.
PD   20-MAR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 274
ID   ABR85707 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049753-A1.
PD   13-MAR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 275
ID   ABR99689 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049763-A1.
PD   13-MAR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 276
ID   ABM00545 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073172-A1.
PD   17-APR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 277
ID   ABM00240 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073172-A1.
PD   17-APR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 278
ID   ABO29672 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068700-A1.
PD   10-APR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 279
ID   ABM23538 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068736-A1.
PD   10-APR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 280
ID   ABM29933 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068679-A1.
PD   10-APR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 281
ID   ABO38264 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068767-A1.
PD   10-APR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 282
ID   ABO45564 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030073182-A1.
PD   17-APR-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 283
ID   ABM20488 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20031004557-A1.
PD   05-JUN-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 284
ID   ADA81337 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030092121-A1.
PD   15-MAY-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 285
ID   ABO16602 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030272276-A1.
PD   06-FEB-2003.
Query Match          100.0%;  Score 1195;  DB 6;  Length 234;

RESULT 286
ID   ABO18228 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044920-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 287
ID   ABO22655 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003027265-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 288
ID   ABO22960 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003054461-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 289
ID   ABR92502 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064446-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 290
ID   ABR81459 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049744-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 291
ID   ABM77883 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049783-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 292
ID   ABR89672 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073171-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 293
ID   ABM26588 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064458-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 294
ID   ABM13714 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032121-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 295
ID   ABO28452 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064460-A1.

RESULT 296
ID   ABO30282 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064464-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 297
ID   ABM07309 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068702-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 298
ID   ABM03900 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068719-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 299
ID   ABO37044 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068734-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 300
ID   ABO41619 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068729-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 301
ID   ABO35214 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068738-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 302
ID   ABM25063 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104540-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 303
ID   ABO47455 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049742-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;  Length 234;

RESULT 304
ID   ABO47760 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049747-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 305
ID ABO48370 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 306
ID ABO51420 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 307
ID ABO51725 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 308
ID ABO50505 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864, SEQ ID NO:66.
PN US20030049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 309
ID ABR79629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030040059-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 310
ID ABM16891 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030040078-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 311
ID ABO17923 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030032132-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 312
ID ABO20875 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030032132-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 313
ID ABR96834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030054462-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 314
ID ABM12189 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030064445-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 315
ID ABM16281 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030064449-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 316
ID ABM24148 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030064441-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 317
ID ABM14629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 318
ID ABO4510 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 319
ID ABO6699 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 320
ID ABO9139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 321
ID ABO39179 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030073174-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 322
ID ABM75444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 6; Pred. No. 1.6e-131; Length 234;

RESULT 323
ID ABM25368 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030104541-A1.
PD 05-JUN-2003.

RESULT 324
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABM19878 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.

RESULT 325
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABO46784 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.

RESULT 326
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABO47089 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.

RESULT 327
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ADA83135 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.

RESULT 328
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABR71520 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.

RESULT 329
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABR72130 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.

RESULT 330
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABO98469 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.

RESULT 331
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABR84792 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.

RESULT 332
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABR73350 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054467-A1.

RESULT 333

PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
RESULT 334
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABR76444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.

RESULT 335
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABR73045 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.

RESULT 336
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABM11111 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.

RESULT 337
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABO20570 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003033126-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.

RESULT 338
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABO25313 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.

RESULT 339
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABO25618 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.

RESULT 340
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABR94027 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.

RESULT 341
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABR79934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.

RESULT 342
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
100.0%; Pred. No. 1.6e-131;
ID ABM11274 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.

RESULT 343

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ID   ABO32801 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030064453-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 344
ID   ABO30587 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030064466-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 345
ID   ABO30892 standard; protein; 234 AA.
DE   Human secreted; protein; 234 AA.
PN   US20030064468-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 346
ID   ABM27198 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068760-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 347
ID   ABM29943 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068769-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 348
ID   ABM05479 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030045700-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 349
ID   ABM15544 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068698-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 350
ID   ABM08529 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049748-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 351
ID   ABO42229 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein 234 AA.
PN   US20030068759-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 352
ID   ABO37959 standard; protein; 234 AA.

DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068765-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 353
ID   ABO45869 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030049754-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 354
ID   ABM66672 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068688-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 355
ID   ADB20178 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030082767-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 356
ID   ABM19573 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104552-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 357
ID   ABO49285 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049774-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 358
ID   ABO49590 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049775-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 359
ID   ADA78430 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030073181-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 360
ID   ABR88147 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068720-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 361
ID   ADA00345 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO 1864.
PN   US20030027992-A1.
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PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 6;  Length 234;
Pred. No. 1.6e-131;

RESULT 362
ID   ABM26893 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068739-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 6;  Length 234;
Pred. No. 1.6e-131;

RESULT 363
ID   ABM03290 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068763-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 6;  Length 234;
Pred. No. 1.6e-131;

RESULT 364
ID   ABO39789 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068689-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 6;  Length 234;
Pred. No. 1.6e-131;

RESULT 365
ID   ABO49895 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049776-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 366
ID   ABO50810 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049780-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 367
ID   ABO05266 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036126-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 368
ID   ABR74570 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044924-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 369
ID   ABR77049 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044927-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 370
ID   ABM17806 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040072-A1.
PD   27-FEB-2003.

RESULT 371
ID   ABR95857 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040073-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 372
ID   ABO21790 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032124-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 373
ID   ABO19960 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054475-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 374
ID   ABO24263 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064467-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 375
ID   ABR86012 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064455-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 376
ID   ABM10664 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049759-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 377
ID   ABM76663 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054465-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 378
ID   ABR93367 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073170-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 379
ID   ABM12494 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073176-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;  Score 1195; DB 7;  Length 234;
Pred. No. 1.6e-131;

RESULT 380
ID   ABM05784 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068717-A1.
PD   10-APR-2003.
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RESULT 381
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABO34909 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068728-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 382
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABM02985 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068764-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 383
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABM18963 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104550-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.

RESULT 384
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABM19268 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104551-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.

RESULT 385
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABO46479 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049761-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 386
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABO48980 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049757-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 387
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABR69023 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027273-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.

RESULT 388
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABR89062 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036119-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

RESULT 389
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABR72435 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036120-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

RESULT 390
Best Local Similarity   100.0%;

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ID   ABR74265 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036161-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

RESULT 391
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABO18533 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044921-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 392
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABR80239 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049739-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 393
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABM01460 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059882-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 394
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABM02070 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059884-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 395
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABR87232 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068687-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 396
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABM12799 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073186-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 397
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABM30553 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064443-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 398
Best Local Similarity   100.0%;
Query Match             100.0%;  Score 1195;  DB 7;   Length 234;
ID   ABM24453 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064444-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 399
Best Local Similarity   100.0%;
ID   ABO29367 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.

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PN   US20030068697-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 400
ID   ABO1197 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein, 234 AA.
PN   US20030068710-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 401
ID   ABM14324 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068686-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 402
ID   ABM09749 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073178-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 403
ID   ABO8874 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068774-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 404
ID   ABM34639 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104538-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 405
ID   ABO5111S standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049781-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 406
ID   ABO10411 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030036151-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 407
ID   ABO3941 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036158-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 408
ID   ABR77654 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030040067-A1.
PD   27-FEB-2003.
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RESULT 409
ID   ABR78864 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054456-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 410
ID   ABO23958 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030054482-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 411
ID   ABR93722 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054457-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 412
ID   ABM01765 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030059883-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 413
ID   ABM78188 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049764-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 414
ID   ABR89977 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073177-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 415
ID   ABM27503 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064442-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 416
ID   ABM13104 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064450-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 417
ID   ABO31807 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068731-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity           100.0%;   Pred. No. 1.6e-131;   Score 1195;   DB 7;   Length 234;
RESULT 418
ID   ABM14019 standard; protein; 234 AA.
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DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030668683-A1.
PD   10-APR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 419
ID   ABM08224 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030668754-A1.
PD   10-APR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 420
ID   ABO40094 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030668681-A1.
PD   10-APR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 421
ID   ABM74529 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030696351-A1.
PD   22-MAY-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 422
ID   ABM33724 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030696358-A1.
PD   22-MAY-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 423
ID   ABM20183 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104556-A1.
PD   05-JUN-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 424
ID   ABO48675 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049756-A1.
PD   13-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 425
ID   ABR72740 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030036122-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 426
ID   ABO15382 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036121-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 427
ID   ABR85097 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030040065-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 428
ID   ABO15077 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030044919-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 429
ID   ABO17212 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030044928-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 430
ID   ABM17501 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030040077-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 431
ID   ABR85402 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049746-A1.
PD   13-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 432
ID   ABM76968 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054464-A1.
PD   20-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 433
ID   ABO28147 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030064459-A1.
PD   03-APR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 434
ID   ABM22928 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030067757-A1.
PD   10-APR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 435
ID   ABM30248 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068723-A1.
PD   10-APR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 436
ID   ABM21708 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068741-A1.
PD   10-APR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 437
ID   ABM21403 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
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PN   US20030068744-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 438
ID   ABM14934 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068766-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 439
ID   ABO41009 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068694-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 440
ID   ABO36739 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068715-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 441
ID   ABO37349 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068726-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 442
ID   ABM75139 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104544-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 443
ID   ABM33419 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030096357-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 444
ID   ABO46174 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030049760-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 445
ID   ADA82501 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049755-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 446
ID   ADB85587 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030049735-A1.

PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 447
ID   ABM31773 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068880-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 448
ID   ADB31163 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068762-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 449
ID   ADB85809 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068708-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 450
ID   ABM32078 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068713-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 451
ID   ABM32383 standard; protein; 234 AA.
DE   Human PRO1864 protein.
PN   US20030065161-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 452
ID   ADB68266 standard; protein; 234 AA.
DE   Human PRO1864 protein.
PN   US20030061600-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 453
ID   ADB68073 standard; protein; 234 AA.
DE   Human PRO1864 protein.
PN   US20030068761-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 454
ID   ABM31468 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068771-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
RESULT 455
ID   ABM30858 standard; protein; 234 AA.

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Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 456
ID   ADB90890 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030083473-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 457
ID   ADC06970 standard; protein; 234 AA.
DE   Novel PRO1864 protein.
PN   US20030060602-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 458
ID   ADC17149 standard; protein; 234 AA.
DE   Mammalian PRO polypeptide (SeqID 14).
PN   US20030065143-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 459
ID   ADC14847 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030073208-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 460
ID   ADC52342 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030138882-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 461
ID   ADD05539 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030087376-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 462
ID   ADD10351 standard; protein; 234 AA.
DE   Human secreted/transmembrane PRO polypeptide #31.
PN   US20030105011-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 463
ID   ADD11311 standard; protein; 234 AA.
DE   Human secreted/transmembrane PRO polypeptide #31.
PN   US20030105013-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 464
ID   ADD37104 standard; protein; 234 AA.
DE   Human secreted/transmembrane PRO polypeptide #31.
PN   US20030105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;

Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 465
ID   ADD36018 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030105296-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 466
ID   ADG01019 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030078387-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 467
ID   ADG08572 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030180793-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 468
ID   ADG02534 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030207397-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 469
ID   ADG01241 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030207399-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 470
ID   ADF95416 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030207398-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 471
ID   ADF95193 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030207392-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 472
ID   ADG12231 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030180918-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;   Pred. No. 1.6e-131;
RESULT 473
ID   ADH24046 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane PRO polypeptide #31.
PN   US20030105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                 100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity       100.0%;
RESULT 474
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RESULT 475
ID   ADH34072 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318080858-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 476
ID   ADH29905 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318080859-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 477
ID   ADH23876 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318080919-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 478
ID   ADH08891 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003207395-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 479
ID   ADG85280 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318090904-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 480
ID   ADH24556 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318090907-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 481
ID   ADH37412 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318081646-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 482
ID   ADH02001 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US200318081648-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 483
ID   ADG85620 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318080905-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 484
ID   ADH24216 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318080914-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 485
ID   ADH38510 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318081643-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 486
ID   ADG83631 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US200318080794-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 487
ID   ADH29439 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318080860-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 488
ID   ADH27555 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318080906-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 489
ID   ADH37752 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318081647-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 490
ID   ADH57349 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318080920-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 491
ID   ADH37929 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318081649-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;
Best Local Similarity   100.0%;
Score 1195;  DB 7;  Length 234;

RESULT 492
ID   ADH53491 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.

PN   US2003181636-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 493
ID   ADH53661 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181641-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 494
ID   ADH51997 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181638-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 495
ID   ADH49852 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181639-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 496
ID   ADH125362 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181696-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 497
ID   ADH90155 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181698-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 498
ID   ADH125532 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181669-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 499
ID   ADH97706 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181672-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 500
ID   ADI03554 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181656-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 501
ID   ADI11911 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003181686-A1.

PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 502
ID   ADH89985 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181697-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 503
ID   ADH98386 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181707-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 504
ID   ADI11061 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003181682-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 505
ID   ADI11571 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003181684-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 506
ID   ADH98216 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181709-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 507
ID   ADH98556 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181708-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 508
ID   ADH98046 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181673-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 509
ID   ADI05034 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180848-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.6e-131;
RESULT 510
ID   ADI03384 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181654-A1.
PD   25-SEP-2003.

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PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 511
ID  ADI04779 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181657-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 512
ID  ADH78233 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181668-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 513
ID  ADI19577 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181676-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 514
ID  ADH90325 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181699-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 515
ID  ADI03044 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181653-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 516
ID  ADH77893 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181666-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 517
ID  ADH97876 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181674-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 518
ID  ADI01261 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003190669-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 519
ID  ADI01956 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181652-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match

RESULT 520
ID  ADI03214 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181655-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 521
ID  ADI11401 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181681-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 522
ID  ADI02303 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181650-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 523
ID  ADI11741 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181685-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 524
ID  ADI05378 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003190716-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 525
ID  ADH79450 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003191290-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 526
ID  ADI19407 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181677-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 527
ID  ADI05208 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181675-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 528
ID  ADH79620 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003191288-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
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Best Local Similarity    100.0%;   Pred. No. 1.6e-131;

RESULT 529
ID   ADI01446 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318678-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 530
ID   ADI01616 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318679-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 531
ID   ADI01786 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318680-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 532
ID   ADH79790 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200319289-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 533
ID   ADI04608 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003171550-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 534
ID   ADI02744 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181651-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 535
ID   ADH78063 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003181667-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 536
ID   ADI25702 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181670-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 537
ID   ADI25872 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181671-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 538
ID   ADK65384 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003073821-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 539
ID   ADH98726 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003191284-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 540
ID   ADH79967 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003191287-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 541
ID   ADL32672 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003207396-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 542
ID   ADM30206 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003073813-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 543
ID   ADL93698 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003040013-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 544
ID   ADC52152 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003130483-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 7;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 545
ID   ADE41312 standard; protein; 234 AA.
DE   Human secreted/transmembrane PRO polypeptide #31.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 8;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 546
ID   ADE74203 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003211572-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1195; DB 8;  Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 547
ID   ADE74815 standard; protein; 234 AA.
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DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20032115574-A1.
PD   13-NOV-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 548
ID   ADF96028 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20032115509-A1.
PD   20-NOV-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 549
ID   ADG04299 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20032155912-A1.
PD   20-NOV-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 550
ID   ADG00459 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20032155911-A1.
PD   20-NOV-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 551
ID   ADH06584 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031808852-A1.
PD   25-SEP-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 552
ID   ADH06414 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031808853-A1.
PD   25-SEP-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 553
ID   ADG68835 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031808855-A1.
PD   25-SEP-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 554
ID   ADH27725 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031808912-A1.
PD   25-SEP-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 555
ID   ADH25066 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031809913-A1.
PD   25-SEP-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 556
ID   ADH33698 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20031816545-A1.
PD   25-SEP-2003.

PA   (GETH ) GENENTECH INC.

RESULT 557
ID   ADG82715 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20032155910-A1.
PD   20-NOV-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 558
ID   ADH02341 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20031808839-A1.
PD   25-SEP-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 559
ID   ADH07948 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031808645-A1.
PD   25-SEP-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 560
ID   ADG69345 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031808846-A1.
PD   25-SEP-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 561
ID   ADH39166 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031808917-A1.
PD   25-SEP-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 562
ID   ADH25996 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031808770-A1.
PD   10-APR-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 563
ID   ADG83906 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20031808842-A1.
PD   04-SEP-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 564
ID   ADG85450 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031666848-A1.
PD   25-SEP-2003.
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
PA   (GETH ) GENENTECH INC.

RESULT 565
ID   ADH06244 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031808854-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 566
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH30074 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031808S6-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 567
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH24386 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180910-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 568
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH32965 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068768-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 569
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADG69515 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180844-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 570
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH07778 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180851-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 571
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADG85790 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180861-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 572
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH39336 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180916-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 573
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH33528 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003181637-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 574
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH33868 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003181644-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 575
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH01078 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003180838-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 576
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADG69685 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180843-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 577
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH02171 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003180841-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 578
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADG69175 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180847-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 579
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADG85960 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180862-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 580
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH24896 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180909-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 581
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH39513 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180915-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 582
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;
ID   ADH02511 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003180849-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 583
Query Match        100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;
ID   ADG69005 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.

RESULT 584
ID ADH07608 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180050-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 585
ID ADG6130 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180908-A1.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 586
ID ADH24726 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180911-A1.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 587
ID ADH25774 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 588
ID ADH38340 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 589
ID ADH57179 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 590
ID ADH43495 standard; protein; 234 AA.
DE Human PRO polypeptide #31.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 591
ID ADH52167 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 592
ID ADH49533 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 593

RESULT 594
ID ADI11231 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 595
ID ADH90495 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 596
ID ADH98896 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190698-A1.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 597
ID ADI02126 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 598
ID ADJ54704 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 599
ID ADH90665 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 600
ID ADJ98540 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 601
ID ADJ98710 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 602
ID ADH78869 standard; protein; 234 AA.

RESULT 602
ID ADJ99103 standard; protein; 234 AA.

DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003186408-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
RESULT 603
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADJ99273 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003187196-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
RESULT 604
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADJ98891 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003187242-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
RESULT 605
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADH79039 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181702-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
RESULT 606
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADK00899 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003186407-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
RESULT 607
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADK14420 standard; protein; 234 AA.
DE   Human PRO polypeptide #31.
PN   US2003187229-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
RESULT 608
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADK82840 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2004043927-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
RESULT 609
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADJ64475 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2004038337-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
RESULT 610
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADM31371 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2004048334-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
RESULT 611
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADM36418 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2004053358-A1.
PD   18-MAR-2004.
PA   (GETH ) GENENTECH INC.
RESULT 612
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADM40223 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2004048335-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
RESULT 613
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADM80669 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2004058411-A1.
PD   25-MAR-2004
PA   (GETH ) GENENTECH INC.
RESULT 614
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADL91873 standard; protein; 234 AA.
DE   Human PRO1864 protein SEQ ID NO:94.
PN   WO2004024076-A2.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
RESULT 615
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADN37831 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2004091959-A1.
PD   13-MAY-2004.
PA   (GETH ) GENENTECH INC.
RESULT 616
Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADY18016 standard; protein; 234 AA.
DE   PRO polypeptide SEQ ID NO 3822.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
RESULT 617
Query Match             100.0%;  Score 1195;  DB 9;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADY13397 standard; protein; 234 AA.
DE   PRO polypeptide SEQ ID NO 5203.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
RESULT 618
Query Match             100.0%;  Score 1195;  DB 9;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   ADY77709 standard; protein; 234 AA.
DE   Neoplastic disease detection protein PRO1864.
PN   US2005059102-A1.
PD   17-MAR-2005.
PA   (EATO/) EATON D L.
PA   (FILV/) FILVAROFF E.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
RESULT 619
Query Match             100.0%;  Score 1195;  DB 9;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
ID   AEA08359 standard; protein; 234 AA.
DE   Steriodogenic acute regulatory protein related (MLN64).
PN   WO2005047536-A2.

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PD   26-MAY-2005.
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS PHARMA GMBH.

RESULT 620
     Best Local Similarity 100.0%;
     Query Match  100.0%;   Score 1195;  DB 9;   Length 234;  Pred. No. 1.6e-131;
ID   AEDS061 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2005163766-A1.
PD   28-JUL-2005.
PA   (GETH ) GENENTECH INC.

RESULT 621
     Best Local Similarity 100.0%;
     Query Match  100.0%;   Score 1195;  DB 9;   Length 234;  Pred. No. 1.6e-131;
ID   AEF12540 standard; protein; 234 AA.
DE   Human PRO1864 protein SEQ ID NO:14.
PN   US2005608901-A1.
PD   12-JAN-2006.
PA   (GETH ) GENENTECH INC.

RESULT 622
     Best Local Similarity 100.0%;
     Query Match  100.0%;   Score 1195;  DB 10;  Length 234;  Pred. No. 1.6e-131;
ID   AEF74229 standard; protein; 234 AA.
DE   Human PRO1864 protein SEQ ID NO:14.
PN   US2005526647-A1.
PD   24-NOV-2005.
PA   (GETH ) GENENTECH INC.
PA   (EATO/) EATON D. L.
PA   (FILV/) FILVAROFF E.
PA   (GERR/) GERRITSEN M. E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P. J.
PA   (GRIM/) GRIMALDI J. C.
PA   (GURN/) GURNEY A. L.
PA   (WATA/) WATANABE C. K.
PA   (WOOD/) WOOD W. L.

RESULT 623
     Best Local Similarity 100.0%;
     Query Match  100.0%;   Score 1195;  DB 10;  Length 238;  Pred. No. 1.7e-131;
ID   AAM41716 standard; protein; 238 AA.
DE   Human polypeptide SEQ ID NO 6647.
PN   WO2001533312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.

RESULT 624
     Best Local Similarity 100.0%;
     Query Match  100.0%;   Score 1195;  DB 4;   Length 238;  Pred. No. 1.7e-131;
ID   AAM41715 standard; protein; 238 AA.
DE   Human polypeptide SEQ ID NO 6646.
PN   WO2001533312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.

RESULT 625
     Best Local Similarity 100.0%;
     Query Match  100.0%;   Score 1195;  DB 4;   Length 238;  Pred. No. 1.7e-131;
ID   ABP75508 standard; protein; 238 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 692.
PN   WO2002883876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.

RESULT 626
     Best Local Similarity 100.0%;
     Query Match  100.0%;   Score 1195;  DB 6;   Length 234;  Pred. No. 1.7e-131;
ID   ABR58404 standard; protein; 234 AA.
DE   Human NOV19b.
PN   WO2003029423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.

RESULT 627
     Best Local Similarity 99.4%;
     Query Match  99.6%;    Score 1188;  DB 6;   Length 234;  Pred. No. 1.1e-130;
ID   AAM39930 standard; protein; 216 AA.
DE   Human polypeptide SEQ ID NO 3075.
PN   WO2001533312-A1.
PD   26-JUL-2001.


RESULT 628
     Best Local Similarity 92.3%;
     Query Match  91.8%;    Score 1097;  DB 4;   Length 216;  Pred. No. 4.9e-120;
ID   ABB90287 standard; protein; 201 AA.
DE   Human polypeptide SEQ ID NO 2663.
PN   WO2001190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.

RESULT 629
     Best Local Similarity 100.0%;
     Query Match  85.7%;    Score 1024;  DB 5;   Length 201;  Pred. No. 1.7e-111;
ID   ABR58403 standard; protein; 198 AA.
DE   Human NOV19a.
PN   WO2003029423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.

RESULT 630
     Best Local Similarity 84.6%;
     Query Match  82.4%;    Score 985;   DB 6;   Length 198;  Pred. No. 6.5e-107;
ID   AAU30250 standard; protein; 283 AA.
DE   Novel human secreted protein #741.
PN   WO2001179449-A2.
PD   25-OCT-2001.
PA   (CURA-) CURAGEN CORP.

RESULT 631
     Best Local Similarity 72.5%;
     Query Match  65.0%;    Score 777;   DB 4;   Length 283;  Pred. No. 3.2e-82;
ID   ADB64413 standard; protein; 176 AA.
DE   Human protein encoded by clone FEBRA20007820.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.

RESULT 632
     Best Local Similarity 87.5%;
     Query Match  56.0%;    Score 669.5; DB 7;   Length 176;  Pred. No. 7.2e-70;
ID   ADK36828 standard; protein; 146 AA.
DE   Novel human polypeptide SeqID8910.
PN   WO2002216439-A2.
PD   28-FEB-2002.
PA   (HYSE-) HYSEQ INC.

RESULT 633
     Best Local Similarity 91.0%;
     Query Match  55.6%;    Score 665;   DB 5;   Length 146;  Pred. No. 1.9e-69;
ID   ADZ88813 standard; protein; 383 AA.
DE   Breast specific protein SEQ ID NO 180.
PN   WO2005044075-A2.
PD   19-MAY-2005.
PA   (DIAD-) DIADEXUS INC.

RESULT 634
     Best Local Similarity 56.2%;
     Query Match  55.6%;    Score 664;   DB 9;   Length 383;  Pred. No. 9.4e-69;
ID   AAW25768 standard; protein; 445 AA.
DE   Human MLN 64.
PN   WO9706256-A2.
PD   20-FEB-1997.
PA   (INRM ) INST NAT SANTE & RECH MEDICALE.
PA   (CNRS ) CENT NAT RECH SCI.
PA   (UYPA-) UNIV PASTEUR LOUIS.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.

RESULT 635
     Best Local Similarity 56.2%;
     Query Match  55.6%;    Score 664;   DB 2;   Length 445;  Pred. No. 1.2e-68;
ID   ABR47530 standard; protein; 445 AA.
DE   Breast cancer associated protein sequence SEQ ID NO:296.
PN   WO2003004989-A2.
PD   16-JAN-2003.
PA   (MILL-) MILLENIUM PHARM INC.

RESULT 636
     Best Local Similarity 56.2%;
     Query Match  55.6%;    Score 664;   DB 6;   Length 445;  Pred. No. 1.2e-68;
ID   ADH13184 standard; protein; 445 AA.
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DE   Human malignant neoplasia-related protein seqID33.
PN   EP1365034-A2.
PD   26-NOV-2003.
PA   (FARB ) BAYER AG.
     Query Match
     Best Local Similarity   55.6%;   56.2%;   Score 664;   DB 8;   Pred. No. 1.2e-68;   Length 445;
RESULT 637
ID   AEA15071 standard; protein; 445 AA.
DE   Human polypeptide #7.
PN   WO200504534-A2.
PD   26-MAY-2005.
PA   (FARB ) BAYER HEALTHCARE AG.
     Query Match
     Best Local Similarity   55.6%;   56.2%;   Score 664;   DB 9;   Pred. No. 1.2e-68;   Length 445;
RESULT 638
ID   ADZ88812 standard; protein; 497 AA.
DE   Breast specific protein SEQ ID NO 179.
PN   WO200504075-A2.
PD   19-MAY-2005.
PA   (DIAD-) DIADEXUS INC.
     Query Match
     Best Local Similarity   55.6%;   56.2%;   Score 664;   DB 9;   Pred. No. 1.4e-68;   Length 497;
RESULT 639
ID   ABG05498 standard; protein; 534 AA.
DE   Novel human diagnostic protein #5489.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match
     Best Local Similarity   52.3%;   48.9%;   Score 625;   DB 4;   Pred. No. 5.8e-64;   Length 534;
RESULT 640
ID   ABR69622 standard; protein; 412 AA.
DE   Human CGDD-22 protein.
PN   WO200302263-A2.
PD   03-APR-2003.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match
     Best Local Similarity   48.4%;   58.3%;   Score 578;   DB 6;   Pred. No. 1.4e-58;   Length 412;
RESULT 641
ID   ABP75900 standard; protein; 111 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 1084.
PN   WO200283876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match
     Best Local Similarity   48.4%;   58.3%;   Score 405.5;   DB 6;   Pred. No. 4.4e-39;   Length 111;
RESULT 642
ID   ABS59968 standard; protein; 580 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 6696.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match
     Best Local Similarity   33.9%;   73.7%;   Score 343;   DB 4;   Pred. No. 9.7e-31;   Length 580;
RESULT 643
ID   AAM90384 standard; protein; 70 AA.
DE   Human immune/haematopoietic antigen SEQ ID NO:17977.
PN   WO200157182-A2.
PD   09-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match
     Best Local Similarity   28.7%;   37.8%;   Score 322;   DB 4;   Pred. No. 1.5e-29;   Length 70;
RESULT 644
ID   AAB96837 standard; protein; 424 AA.
DE   Putative P. abyssi nucleoside-diphosphate-sugar pyrophosphorylase #6.
PN   FR279651-A1.
PD   27-OCT-2000.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
PA   (IFRE-) IFREMER INST FR RECH EXPL MER.
     Query Match
     Best Local Similarity   7.8%;   21.9%;   Score 93.5;   DB 4;   Pred. No. 0.14;   Length 424;
RESULT 645
ID   AAU03699 standard; protein; 373 AA.
DE   Group B Streptococcus antigenic protein, ID-176.
PN   WO200132882-A2.
PD   10-MAY-2001.
PA   (MICR-) MICROBIAL TECHNICS LTD.
     Query Match
     Best Local Similarity   7.6%;   25.7%;   Score 91;   DB 4;   Pred. No. 0.23;   Length 373;
RESULT 646
ID   ADV89705 standard; protein; 605 AA.
DE   Streptococcus agalactiae protein, SEQ ID 2099.
PN   FR2824074-A1.
PD   31-OCT-2002.
PA   (CNRS ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match
     Best Local Similarity   7.6%;   25.7%;   Score 91;   DB 8;   Pred. No. 0.46;   Length 605;
RESULT 647
ID   ADV80958 standard; protein; 605 AA.
DE   Streptococcus agalactiae protein sequence, SEQ ID 2099.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (CNRS ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match
     Best Local Similarity   7.6%;   25.7%;   Score 91;   DB 8;   Pred. No. 0.46;   Length 605;
RESULT 648
ID   ABP30317 standard; protein; 651 AA.
DE   Streptococcus agalactiae polypeptide SEQ ID NO 9810.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match
     Best Local Similarity   7.6%;   25.7%;   Score 91;   DB 5;   Pred. No. 0.5;   Length 651;
RESULT 649
ID   ADV83104 standard; protein; 651 AA.
DE   Streptococcus agalactiae protein, SEQ ID 4245.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (CNRS ) INST PASTEUR.
     Query Match
     Best Local Similarity   7.6%;   25.7%;   Score 91;   DB 8;   Pred. No. 0.5;   Length 651;
RESULT 650
ID   ABP29732 standard; protein; 654 AA.
DE   Streptococcus polypeptide SEQ ID NO 8640.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match
     Best Local Similarity   7.6%;   25.7%;   Score 91;   DB 5;   Pred. No. 0.51;   Length 654;
RESULT 651
ID   ABP26469 standard; protein; 654 AA.
DE   Streptococcus polypeptide SEQ ID NO 2114.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match
     Best Local Similarity   7.6%;   25.7%;   Score 91;   DB 5;   Pred. No. 0.51;   Length 654;
RESULT 652
ID   AAG61678 standard; protein; 155 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO 80037.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match
     Best Local Similarity   7.3%;   21.4%;   Score 87.5;   DB 3;   Pred. No. 0.18;   Length 155;
RESULT 653
ID   AAG59838 standard; protein; 155 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 77441.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match
     Best Local Similarity   7.3%;   21.4%;   Score 87.5;   DB 3;   Pred. No. 0.18;   Length 155;
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Best Local Similarity   21.4%;   Pred. No. 0.18;

RESULT 654
ID   AAB58945 standard; protein; 516 AA.
DE   Breast and ovarian cancer associated antigen protein sequence SEQ ID 653.
PN   WO200055173-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match
     Best Local Similarity   23.7%;   Pred. No. 0.94;   Score 87;   DB 3;   Length 516;

RESULT 655
ID   ADQ39266 standard; protein; 421 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 929.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   25.2%;   Pred. No. 0.81;   Score 85.5;   DB 8;   Length 421;

RESULT 656
ID   ADQ39263 standard; protein; 223 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 926.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   25.2%;   Pred. No. 0.71;   Score 85.5;   DB 8;   Length 223;

RESULT 657
ID   ADQ39258 standard; protein; 285 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 921.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 0.51;   Score 85.5;   DB 8;   Length 285;

RESULT 658
ID   ADQ39262 standard; protein; 315 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 925.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 0.82;   Score 85.5;   DB 8;   Length 315;

RESULT 659
ID   ADQ39260 standard; protein; 323 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 923.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 0.85;   Score 85.5;   DB 8;   Length 323;

RESULT 660
ID   ADQ39261 standard; protein; 328 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 924.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 0.86;   Score 85.5;   DB 8;   Length 328;

RESULT 661
ID   ADQ39265 standard; protein; 338 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 928.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 0.9;   Score 85.5;   DB 8;   Length 338;

RESULT 662
ID   ADQ39267 standard; protein; 339 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 930.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 0.9;   Score 85.5;   DB 8;   Length 339;

RESULT 663
ID   ADE28099 standard; protein; 340 AA.
DE   Human NTRAN protein - SEQ ID 4.
PN   WO2003051902-A1.
PD   26-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 0.91;   Score 85.5;   DB 7;   Length 340;

RESULT 664
ID   ADQ39269 standard; protein; 384 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 932.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 1.1;   Score 85.5;   DB 8;   Length 384;

RESULT 665
ID   ADQ39264 standard; protein; 390 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 927.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 1.1;   Score 85.5;   DB 8;   Length 390;

RESULT 666
ID   ABU26680 standard; protein; 396 AA.
DE   Protein encoded by Prokaryotic essential gene #12207.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match
     Best Local Similarity   21.0%;   Pred. No. 1.1;   Score 85.5;   DB 6;   Length 396;

RESULT 667
ID   AAW13575 standard; protein; 438 AA.
DE   Batten disease polypeptide CLN3.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 1.1;   Score 85.5;   DB 2;   Length 438;

RESULT 668
ID   AAW13589 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L204.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 1.3;   Score 85.5;   DB 2;   Length 438;

RESULT 669
ID   AAW13582 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L46.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match
     Best Local Similarity   24.8%;   Pred. No. 1.3;   Score 85.5;   DB 2;   Length 438;

RESULT 670
ID   AAW13577 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L39.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 1.3;   Score 85.5;   DB 2;   Length 438;

RESULT 671
ID   ADQ96392 standard; protein; 438 AA.
DE   T cell activation associated protein #285.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   25.5%;   Pred. No. 1.3;   Score 85.5;   DB 2;   Length 438;
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PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match        7.2%;   Score 25.5%;
     Best Local Similarity   25.5%;   Pred. No. 1.3;
RESULT 672
ID   ADQ39268 standard; protein; 438 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 931.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match        7.2%;   Score 25.5%;   DB 8;   Length 438;
     Best Local Similarity   25.5%;   Pred. No. 1.3;
PA   (CURA-) CURAGEN CORP.
PD   10-APR-2003.
PN   WO2003029424-A2.
DE   Human NOV43a protein SEQ ID NO:182.
ID   ADA05822 standard; protein; 440 AA.
RESULT 673
     Best Local Similarity   25.2%;   Pred. No. 1.3;
     Query Match        7.2%;   Score 85.5;   DB 6;   Length 440;
PA   (CURA-) CURAGEN CORP.
US20040038223-A1.
ID   ADN63244 standard; protein; 440 AA.
DE   Human NOV43a variant.
US20040038223-A1.
26-FEB-2004.
RESULT 674
     Best Local Similarity   25.2%;   Pred. No. 1.3;
     Query Match        7.2%;   Score 85.5;   DB 8;   Length 440;
ID   ADN62985 standard; protein; 440 AA.
DE   Human NOV43a.
US20040038223-A1.
26-FEB-2004.
RESULT 675
     Best Local Similarity   25.2%;   Pred. No. 1.3;
     Query Match        7.2%;   Score 85.5;   DB 8;   Length 440;
PA   (SMIT/) SMITHSON G.
PA   (MILL/) MILLET I.
PA   (PEYM/) PEYMAN J A.
PA   (KEKU/) KEKUDA R.
PA   (JUJJ/) JU J.
PA   (LILL/) LI L.
PA   (GUOX/) GUO X.
PA   (PATT/) PATTURAJAN M.
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PA   (SPYT/) SPYTEK K A.
PA   (EDIN/) EDINGER S R.
PA   (ELLE/) ELLERMAN K.
PA   (MALY/) MALYANKAR U M.
PA   (ORTT/) ORT T.
PA   (GORM/) GORMAN L.
PA   (ZERH/) ZERHUSEN B D.
PA   (ANDE/) ANDERSON D W.
PA   (ZHON/) ZHONG M.
PA   (CATT/) CATTERTON E.
PA   (JIWW/) JI W.
PA   (MILL/) MILLER C E.
PA   (RAST/) RASTELLI L.
PA   (STON/) STONE D J.
PA   (PENA/) PENA C E A.
PA   (EISE/) EISEN A.
PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (ROTH/) ROTHENBERG M E.
PA   (LEAC/) LEACH M D.
PA   (AGEE/) AGEE M L.
PA   (BERG/) BERGHS C.
PA   (DIPI/) DIPIPPO V A.
PA   (EISE/) EISEN A.
PA   (GANG/) GANGOLLI E A.
PA   (RIEG/) RIEGER D K.
PA   (SPAD/) SPADERNA S K.
     Query Match        7.2%;   Score 25.5%;   DB 8;   Length 440;
     Best Local Similarity   25.5%;   Pred. No. 1.3;
RESULT 676
ID   AED74247 standard; protein; 449 AA.
DE   Human placental protein SEQ ID NO:1075.
PN   US20050255114-A1.
PD   17-NOV-2005.
PA   (NUVE-) NUVELO INC.
     Query Match        7.2%;   Score 85.5;   DB 9;   Length 449;
     Best Local Similarity   25.5%;   Pred. No. 1.3;
RESULT 677
ID   AAW13593 standard; protein; 467 AA.
DE   Batten disease CLN3 mutant protein in family L61.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match        7.2%;   Score 85.5;   DB 2;   Length 467;
     Best Local Similarity   25.5%;   Pred. No. 1.4;
RESULT 678
ID   ABB89640 standard; protein; 473 AA.
DE   Human polypeptide SEQ ID NO 2016.
PN   WO2001090304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match        7.2%;   Score 85.5;   DB 5;   Length 473;
     Best Local Similarity   25.2%;   Pred. No. 1.4;
RESULT 679
ID   ADQ18055 standard; protein; 473 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 872.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match        7.2%;   Score 85.5;   DB 8;   Length 473;
     Best Local Similarity   25.2%;   Pred. No. 1.4;
RESULT 680
ID   ADU06406 standard; protein; 473 AA.
DE   Novel bronchial cancer-associated human protein SeqID630.
PN   DE10316701-A1.
PD   04-NOV-2004.
PA   (HINZ/) HINZMANN B.
PA   (HERM/) HERMANN K.
PA   (CAST/) HEIDEN CASTANOS-VELEZ E.
     Query Match        7.2%;   Score 85.5;   DB 8;   Length 473;
     Best Local Similarity   25.2%;   Pred. No. 1.4;
RESULT 681
ID   ADY20253 standard; protein; 473 AA.
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DE   PRO polypeptide SEQ ID NO 6059.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
RESULT 682
Best Local Similarity      25.2%;
ID   ABU40544 standard; protein; 500 AA.
DE   Protein encoded by Prokaryotic essential gene #26071.
PN   WO2002077183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
RESULT 683
Query Match      7.2%;      Score 85.5;   DB 9;   Length 473;
Best Local Similarity      26.0%;
ID   ADY09432 standard; protein; 527 AA.
DE   Plant full length insert polypeptide seqid 65247.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
RESULT 684
Query Match      7.1%;      Score 85;     DB 8;   Length 527;
Best Local Similarity      17.6%;
ID   ABU33210 standard; protein; 430 AA.
DE   Protein encoded by Prokaryotic essential gene #18737.
PN   WO2002077183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
RESULT 685
Query Match      7.1%;      Score 84.5;   DB 6;   Length 430;
Best Local Similarity      25.5%;
ID   AAW13588 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L10.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
RESULT 686
Query Match      7.1%;      Score 84.5;   DB 2;   Length 438;
Best Local Similarity      24.8%;
ID   AAG16921 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 17749.
PN   EP1033405-A2.
PD   06-SEP-2000.
RESULT 687
Query Match      7.0%;      Score 83.5;   DB 3;   Length 322;
Best Local Similarity      33.7%;
ID   ABG21285 standard; protein; 472 AA.
DE   Novel human diagnostic protein #21276.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
RESULT 688
Query Match      7.0%;      Score 83.5;   DB 4;   Length 472;
Best Local Similarity      20.1%;
ID   ABU35608 standard; protein; 239 AA.
DE   Protein encoded by Prokaryotic essential gene #21135.
PN   WO2002077183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
RESULT 689
Query Match      6.9%;      Score 82.5;   DB 6;   Length 239;
Best Local Similarity      21.7%;
ID   ADU25550 standard; protein; 389 AA.
DE   L. acidophilus cell surface protein homologue #63.
PN   WO2004096992-A2.
PD   11-NOV-2004.
PA   (UYNC-) UNIV NORTH CAROLINA STATE.

Query Match      6.9%;      Score 82.5;   DB 8;   Length 389;
Best Local Similarity      24.7%;
ID   AAW13590 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L216.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
RESULT 690
Query Match      6.9%;      Score 82;     DB 7;   Length 438;
Best Local Similarity      19.5%;
ID   ADX74800 standard; protein; 264 AA.
DE   Plant full length insert polypeptide seqid 44166.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
RESULT 691
Query Match      6.9%;      Score 82;     DB 2;   Length 264;
Best Local Similarity      24.8%;
ID   ADB85263 standard; protein; 589 AA.
DE   Mouse RNA1 homologue SEQ ID NO:144.
PN   EP1284297-A2.
PD   19-FEB-2003.
PA   (WARN ) WARNER LAMBERT CO.
RESULT 692
Query Match      6.8%;      Score 81.5;   DB 7;   Length 589;
Best Local Similarity      19.5%;
ID   AAW13586 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L285.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
RESULT 693
Query Match      6.8%;      Score 81.5;   DB 2;   Length 438;
Best Local Similarity      24.8%;
ID   AAB92924 standard; protein; 519 AA.
DE   Human protein sequence SEQ ID NO:11574.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
RESULT 694
Query Match      6.8%;      Score 81.5;   DB 4;   Length 519;
Best Local Similarity      22.6%;
ID   ADE28193 standard; protein; 577 AA.
DE   Human MDDT protein - SEQ ID 43.
PN   WO2003046152-A2.
PD   05-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
RESULT 695
Query Match      6.8%;      Score 81.5;   DB 5;   Length 577;
Best Local Similarity      22.6%;
ID   ADN23155 standard; protein; 529 AA.
DE   Bacterial polypeptide #5808.
PN   US2002233675-A1.
PD   18-DEC-2003.
PA   (HINK/) HINKLE G J.
PA   (CAOY/) CAO Y.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
RESULT 696
Query Match      6.8%;      Score 81.5;   DB 7;   Length 529;
Best Local Similarity      23.1%;
ID   ADN23156 standard; protein; 529 AA.
DE   Bacterial polypeptide #5809.
PN   US2002233675-A1.
RESULT 697

PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match      6.8%;   Score 81;   DB 8;   Length 529;
Best Local Similarity   23.1%;   Pred. No. 5.7;

RESULT 698
ID   AAG53771 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68491.
PN   EP103405-A2.
PD   06-SEP-2000.
Query Match      6.7%;   Score 80.5;   DB 3;   Length 322;
Best Local Similarity   32.7%;   Pred. No. 3.3;

RESULT 699
ID   AAG25639 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 29783.
PN   EP103405-A2.
PD   06-SEP-2000.
Query Match      6.7%;   Score 80.5;   DB 3;   Length 322;
Best Local Similarity   32.7%;   Pred. No. 3.3;

RESULT 700
ID   AAG53746 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68457.
PN   EP103405-A2.
PD   06-SEP-2000.
Query Match      6.7%;   Score 80.5;   DB 3;   Length 322;
Best Local Similarity   32.7%;   Pred. No. 3.3;

RESULT 701
ID   AB063194 standard; protein; 350 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9711.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match      6.7%;   Score 80.5;   DB 7;   Length 350;
Best Local Similarity   31.8%;   Pred. No. 3.7;

RESULT 702
ID   ABB48552 standard; protein; 463 AA.
DE   Listeria monocytogenes protein #1256.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP-) INST PASTEUR.
Query Match      6.7%;   Score 80.5;   DB 5;   Length 463;
Best Local Similarity   19.0%;   Pred. No. 5.4;

RESULT 703
ID   ABU33036 standard; protein; 463 AA.
DE   Protein encoded by Prokaryotic essential gene #18563.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match      6.7%;   Score 80.5;   DB 6;   Length 463;
Best Local Similarity   19.0%;   Pred. No. 5.4;

RESULT 704
ID   ADD43870 standard; protein; 536 AA.
DE   Chlamydia trachomatis immunogenic protein, SEQ ID No 165.
PN   WO2003049762-A2.
PD   19-JUN-2003.
PA   (CHIR-) CHIRON SPA.
Query Match      6.7%;   Score 80.5;   DB 7;   Length 536;
Best Local Similarity   25.2%;   Pred. No. 6.6;

RESULT 705
ID   AEA19162 standard; protein; 536 AA.
DE   Chlamydia trachomatis protein - SEQ ID 165.
PN   US2005106162-A1.
PD   19-MAY-2005.
PA   (GRAN/) GRANDI G.
PA   (RATT/) RATTI G.
Query Match      6.7%;   Score 80.5;   DB 9;   Length 536;
Best Local Similarity   25.2%;   Pred. No. 6.6;

RESULT 706
ID   ADC42920 standard; protein; 891 AA.
DE   Vaccinia Virus Major Core protein P4a precursor.

PN   WO2003017943-A2.
PD   06-MAR-2003.
PA   (MYRI-) MYRIAD GENETICS INC.
Query Match      6.7%;   Score 80.5;   DB 7;   Length 891;
Best Local Similarity   23.3%;   Pred. No. 13;

RESULT 707
ID   ABB92830 standard; protein; 1780 AA.
DE   Herbicidally active polypeptide SEQ ID NO 2041.
PN   WO200210210-A2.
PD   07-FEB-2002.
PA   (FARB ) BAYER AG.
Query Match      6.7%;   Score 80.5;   DB 5;   Length 1780;
Best Local Similarity   20.8%;   Pred. No. 35;

RESULT 708
ID   AEB31016 standard; protein; 1780 AA.
DE   Arabidopsis thaliana glucan synthase-like protein-5.
PN   WO200511215-A2.
PD   24-NOV-2005.
PA   (BADI ) BASF PLANT SCI GMBH.
Query Match      6.7%;   Score 80.5;   DB 9;   Length 1780;
Best Local Similarity   20.8%;   Pred. No. 35;

RESULT 709
ID   AAB54399 standard; protein; 144 AA.
DE   Human pancreatic cancer antigen protein sequence SEQ ID NO:851.
PN   WO200055320-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match      6.7%;   Score 80.5;   DB 3;   Length 144;
Best Local Similarity   25.4%;   Pred. No. 1.2;

RESULT 710
ID   AAM39952 standard; protein; 238 AA.
DE   Human polypeptide SEQ ID NO 3097.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
Query Match      6.7%;   Score 80;   DB 4;   Length 238;
Best Local Similarity   22.5%;   Pred. No. 2.5;

RESULT 711
ID   ADM04473 standard; protein; 238 AA.
DE   Human protein of the invention SEQ ID NO:3158.
PN   EP1347046-A1.
PD   24-SEP-2003.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match      6.7%;   Score 80;   DB 7;   Length 238;
Best Local Similarity   22.5%;   Pred. No. 2.5;

RESULT 712
ID   AEC87403 standard; protein; 238 AA.
DE   Human cDNA clone protein D9OST20002780, SEQ ID 3158.
PN   EP1580263-A1.
PD   28-SEP-2005.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match      6.7%;   Score 80;   DB 9;   Length 238;
Best Local Similarity   22.5%;   Pred. No. 2.5;

RESULT 713
ID   AAM41738 standard; protein; 249 AA.
DE   Human polypeptide SEQ ID NO 6669.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
Query Match      6.7%;   Score 80;   DB 4;   Length 249;
Best Local Similarity   22.5%;   Pred. No. 2.6;

RESULT 714
ID   AAR77844 standard; protein; 309 AA.
DE   Molasses toxicity resistance protein RTM1.
PN   WO9514774-A1.
PD   01-JUN-1995.
PA   (CNRS ) CENT NAT RECH SCI.
Query Match      6.7%;   Score 80;   DB 2;   Length 309;
Best Local Similarity   28.0%;   Pred. No. 3.5;

RESULT 715
ID   ABM67388 standard; protein; 330 AA.
DE   Photorhabdus luminescens protein sequence #485.
PN   WO200294867-A2.

PD 28-NOV-2002.
PA (INSP ) INST PASTEUR.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 24.6%; Pred. No. 3.9; Score 80; DB 6; Length 330;

RESULT 716
ID AAE03831 standard; protein; 360 AA.
DE Human gene 14 encoded secreted protein HDQFN31, SEQ ID NO: 77.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity 22.5%; Pred. No. 4.4; Score 80; DB 4; Length 360;

RESULT 717
ID ABG64559 standard; protein; 360 AA.
DE Human albumin fusion protein #1234.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity 22.5%; Pred. No. 4.4; Score 80; DB 5; Length 360;

RESULT 718
ID ADL77826 standard; protein; 360 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1308.
PN US200401013-A1.
PD 15-JAN-2004.
PA (HASE/) HASELTINE W A.
Best Local Similarity 22.5%; Pred. No. 4.4; Score 80; DB 8; Length 360;

RESULT 719
ID ADX62260 standard; protein; 516 AA.
DE Plant full length insert polypeptide seqid 37103.
PN US200403488-A1.
PD 19-FEB-2004.
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 20.0%; Pred. No. 7.2; Score 80; DB 8; Length 516;

RESULT 720
ID ABU25554 standard; protein; 365 AA.
DE Protein encoded by Prokaryotic essential gene #11081.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 21.2%; Pred. No. 5.1; Score 79.5; DB 6; Length 365;

RESULT 721
ID AARS8703 standard; protein; 406 AA.
DE HCMV IE-exon-4 subunit.
PN WO9417810-A1.
PD 18-AUG-1994.
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
Query Match
Best Local Similarity 19.3%; Pred. No. 5.9; Score 79.5; DB 2; Length 406;

RESULT 722
ID AAW27275 standard; protein; 406 AA.
DE Human cytomegalovirus immediate-early exon 4 product.
PN WO9740165-A1.
PD 30-OCT-1997.
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
Query Match
Best Local Similarity 19.3%; Pred. No. 5.9; Score 79.5; DB 2; Length 406;

RESULT 723
ID ABB58483 standard; protein; 638 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2241.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.

Query Match
Best Local Similarity 20.5%; Pred. No. 11; Score 79.5; DB 4; Length 638;

RESULT 724
ID AAE13277 standard; protein; 723 AA.
DE Human transporters and ion channels (TRICH)-4.
PN WO200177174-A2.
PD 18-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 18.0%; Pred. No. 13; Score 79.5; DB 5; Length 723;

RESULT 725
ID ADL12774 standard; protein; 723 AA.
DE Human steroid-induced C3A liver cell protein #80.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity 18.0%; Pred. No. 13; Score 79.5; DB 8; Length 723;

RESULT 726
ID AAW20696 standard; protein; 121 AA.
DE H. pylori secreted or periplasmic protein 05ae202200rf50.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR ) ASTRA AB.
Query Match
Best Local Similarity 21.4%; Pred. No. 1.3; Score 79.5; DB 2; Length 121;

RESULT 727
ID ABB60462 standard; protein; 323 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8178.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 18.8%; Pred. No. 4.9; Score 79; DB 4; Length 323;

RESULT 728
ID AEB41478 standard; protein; 356 AA.
DE L. pneumophila protein SEQ ID NO 5810.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP ) INST PASTEUR.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Best Local Similarity 23.0%; Pred. No. 5.6; Score 79; DB 9; Length 356;

RESULT 729
ID AEB38189 standard; protein; 358 AA.
DE L. pneumophila protein SEQ ID NO 2521.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP ) INST PASTEUR.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 23.0%; Pred. No. 5.7; Score 79; DB 9; Length 358;

RESULT 730
ID ABR58610 standard; protein; 1531 AA.
DE Human cancer related protein SEQ ID NO:267.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 24.3%; Pred. No. 43; Score 79; DB 6; Length 1531;

RESULT 731
ID ADB31753 standard; protein; 1531 AA.
DE Human 59590 protein #SEQ ID 110.
PN WO2003065984-A2.
PD 14-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 24.3%; Pred. No. 43; Score 79; DB 7; Length 1531;

RESULT 732

ID   AEF11993 standard; protein; 1531 AA.
DE   Human heart alpha-kinase protein SEQ ID NO 2.
PN   WO2005124359-A2.
PD   29-DEC-2005.
PA   (META-) METABOLEX INC.
RESULT 733
     Query Match   24.3%;
     Best Local Similarity
          Score 79; DB 10; Length 1531;
          Pred. No. 43;

ID   AEF11995 standard; protein; 1536 AA.
DE   Human heart alpha-kinase Metabolex variant protein SEQ ID NO 4.
PN   WO2005124359-A2.
PD   29-DEC-2005.
PA   (META-) METABOLEX INC.
RESULT 734
     Query Match   24.3%;
     Best Local Similarity
          Score 79; DB 10; Length 1536;
          Pred. No. 43;

ID   ABU62069 standard; protein; 1597 AA.
DE   Human heart alpha-kinase (HK).
PN   US2002177205-A1.
PD   28-NOV-2002.
PA   (RYAZ/) RYAZANOV A.
RESULT 735
     Query Match   24.3%;
     Best Local Similarity
          Score 79; DB 6; Length 1597;
          Pred. No. 45;

ID   ABU62070 standard; protein; 1597 AA.
DE   Mouse heart alpha-kinase (HK).
PN   US2002177205-A1.
PD   28-NOV-2002.
PA   (RYAZ/) RYAZANOV A.
RESULT 736
     Query Match   24.3%;
     Best Local Similarity
          Score 79; DB 6; Length 1597;
          Pred. No. 45;

ID   ABO55689 standard; protein; 135 AA.
DE   Human genome derived single exon protein #1923.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
RESULT 737
     Query Match   59.4%;
     Best Local Similarity
          Score 78.5; DB 8; Length 135;
          Pred. No. 1.7;

ID   ADU02890 standard; protein; 165 AA.
DE   Novel human polypeptide seqid 1357.
PN   WO2004093804-A2.
PD   04-NOV-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
RESULT 738
     Query Match   24.6%;
     Best Local Similarity
          Score 78.5; DB 8; Length 165;
          Pred. No. 2.2;

ID   AEB38367 standard; protein; 205 AA.
DE   L. pneumophila protein SEQ ID NO 2699.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP) INST PASTEUR.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS) CNRS CENT NAT RECH SCI.
RESULT 739
     Query Match   18.3%;
     Best Local Similarity
          Score 78.5; DB 9; Length 205;
          Pred. No. 3;

ID   ADB10816 standard; protein; 228 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO:4244.
PN   WO2003048304-A2.
PD   12-JUN-2003.
PA   (AMHP) WYETH HOLDINGS CORP.
RESULT 740
     Query Match   22.5%;
     Best Local Similarity
          Score 78.5; DB 6; Length 228;
          Pred. No. 3.5;

ID   ABU36298 standard; protein; 239 AA.
DE   Protein encoded by Prokaryotic essential gene #21825.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
RESULT 741
     Query Match   23.4%;
     Best Local Similarity
          Score 78.5; DB 6; Length 239;
          Pred. No. 3.7;

ID   ADJ27174 standard; protein; 626 AA.
DE   Human TRICH-6, SEQ ID 6.
PN   WO2004013293-A2.
PD   12-FEB-2004.
PA   (INCY-) INCYTE CORP.
RESULT 742
     Query Match   18.0%;
     Best Local Similarity
          Score 78.5; DB 8; Length 626;
          Pred. No. 14;

ID   ABM84879 standard; protein; 648 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:5128.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
RESULT 743
     Query Match   18.0%;
     Best Local Similarity
          Score 78.5; DB 8; Length 648;
          Pred. No. 15;

ID   ABM84877 standard; protein; 668 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:5126.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
RESULT 744
     Query Match   18.0%;
     Best Local Similarity
          Score 78.5; DB 8; Length 668;
          Pred. No. 15;

ID   ABP29904 standard; protein; 669 AA.
DE   Streptococcus polypeptide SEQ ID NO 8984.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
RESULT 745
     Query Match   23.5%;
     Best Local Similarity
          Score 78.5; DB 5; Length 669;
          Pred. No. 15;

ID   ABP28724 standard; protein; 669 AA.
DE   Streptococcus polypeptide SEQ ID NO 6624.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
RESULT 746
     Query Match   23.5%;
     Best Local Similarity
          Score 78.5; DB 5; Length 669;
          Pred. No. 15;

ID   ADI21047 standard; protein; 703 AA.
DE   Novel human protein #22.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
RESULT 747
     Query Match   18.0%;
     Best Local Similarity
          Score 78.5; DB 7; Length 703;
          Pred. No. 17;

ID   AEM84882 standard; protein; 711 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:5131.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
RESULT 748
     Query Match   18.0%;
     Best Local Similarity
          Score 78.5; DB 8; Length 711;
          Pred. No. 17;

ID   ABP52105 standard; protein; 723 AA.
DE   Homo sapiens ABC transporter ABCB9 protein SEQ ID NO:57.
PN   EP1217066-A1.
PD   26-JUN-2002.
PA   (UYGE-) UNIV GENT.
RESULT 749
     Query Match   18.0%;
     Best Local Similarity
          Score 78.5; DB 5; Length 723;
          Pred. No. 17;

ID   ADQ97094 standard; protein; 723 AA.
DE   Human cancer associated sequence HP1-10-005, SEQ ID 70.
PN   WO2004060304-A2.

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PD  22-JUL-2004.
PA  (SAGR-) SAGRES DISCOVERY INC.
    Query Match                  6.6%;  Score 78.5;  DB 8;  Length 723;
    Best Local Similarity  18.0%;  Pred. No. 17;
RESULT 750
ID  AAE02437 standard; protein; 766 AA.
DE  Human ATP binding cassette, ABCB9 transporter protein.
PN  WO200140305-A1.
PD  07-JUN-2001.
PA  (ACTI-) ACTIVE PASS PHARM INC.
    Query Match                  6.6%;  Score 78.5;  DB 4;  Length 766;
    Best Local Similarity  18.0%;  Pred. No. 19;
RESULT 751
ID  AAE02441 standard; protein; 766 AA.
DE  Human ATP binding cassette, ABCB9 transporter protein mutant K545R.
PN  WO200140305-A1.
PD  07-JUN-2001.
PA  (ACTI-) ACTIVE PASS PHARM INC.
    Query Match                  6.6%;  Score 78.5;  DB 4;  Length 766;
    Best Local Similarity  18.0%;  Pred. No. 19;
RESULT 752
ID  AAE02442 standard; protein; 766 AA.
DE  Human ATP binding cassette, ABCB9 transporter protein mutant D667N.
PN  WO200140305-A1.
PD  07-JUN-2001.
PA  (ACTI-) ACTIVE PASS PHARM INC.
    Query Match                  6.6%;  Score 78.5;  DB 4;  Length 766;
    Best Local Similarity  18.0%;  Pred. No. 19;
RESULT 753
ID  AAG67163 standard; protein; 766 AA.
DE  Amino acid sequence of a human 33894 transporter polypeptide.
PN  WO200164875-A2.
PD  07-SEP-2001.
PA  (MILL-) MILLENNIUM PHARM INC.
    Query Match                  6.6%;  Score 78.5;  DB 4;  Length 766;
    Best Local Similarity  18.0%;  Pred. No. 19;
RESULT 754
ID  AAG79246 standard; protein; 766 AA.
DE  Amino acid sequence of a human TAP-like (HUTAPL) polypeptide.
PN  WO200173018-A2.
PD  04-OCT-2001.
PA  (MERE ) MERCK PATENT GMBH.
    Query Match                  6.6%;  Score 78.5;  DB 4;  Length 766;
    Best Local Similarity  18.0%;  Pred. No. 19;
RESULT 755
ID  ABB98345 standard; protein; 766 AA.
DE  Human ABC transporter ABCB9 SEQ ID NO 6.
PN  WO200264781-A2.
PD  22-AUG-2002.
PA  (ACTI-) ACTIVE PASS PHARM INC.
    Query Match                  6.6%;  Score 78.5;  DB 5;  Length 766;
    Best Local Similarity  18.0%;  Pred. No. 19;
RESULT 756
ID  AAE22170 standard; protein; 766 AA.
DE  Human TRICH-14 protein.
PN  WO200212340-A2.
PD  14-FEB-2002.
PA  (INCY-) INCYTE GENOMICS INC.
    Query Match                  6.6%;  Score 78.5;  DB 5;  Length 766;
    Best Local Similarity  18.0%;  Pred. No. 19;
RESULT 757
ID  ADQ97096 standard; protein; 766 AA.
DE  Human cancer associated sequence HP2-10-005, SEQ ID 72.
PN  WO200406304-A2.
PD  22-JUL-2004.
PA  (SAGR-) SAGRES DISCOVERY INC.
    Query Match                  6.6%;  Score 78.5;  DB 8;  Length 766;
    Best Local Similarity  18.0%;  Pred. No. 19;
RESULT 758
ID  AAG20805 standard; protein; 377 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 23131.
PN  EP1033405-A2.
PD  06-SEP-2000.
    Query Match                  6.5%;  Score 78;  DB 3;  Length 377;
    Best Local Similarity  23.8%;  Pred. No. 8;
RESULT 759
ID  AAG20804 standard; protein; 442 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 23130.
PN  EP1033405-A2.
PD  06-SEP-2000.
PA  (ELIT-) ELITRA PHARM INC.
    Query Match                  6.5%;  Score 78;  DB 3;  Length 442;
    Best Local Similarity  23.8%;  Pred. No. 10;
RESULT 760
ID  AAU35545 standard; protein; 471 AA.
DE  Haemophilus influenzae cellular proliferation protein #186.
PN  WO200170955-A2.
PD  27-SEP-2001.
PA  (ELIT-) ELITRA PHARM INC.
    Query Match                  6.5%;  Score 78;  DB 4;  Length 471;
    Best Local Similarity  25.0%;  Pred. No. 11;
RESULT 761
ID  ABU30411 standard; protein; 471 AA.
DE  Protein encoded by Prokaryotic essential gene #15938.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
    Query Match                  6.5%;  Score 78;  DB 4;  Length 471;
    Best Local Similarity  25.0%;  Pred. No. 11;
RESULT 762
ID  AAG20803 standard; protein; 489 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 23129.
PN  EP1033405-A2.
PD  06-SEP-2000.
    Query Match                  6.5%;  Score 78;  DB 3;  Length 489;
    Best Local Similarity  23.8%;  Pred. No. 11;
RESULT 763
ID  ABB49039 standard; protein; 269 AA.
DE  Listeria monocytogenes protein #1743.
PN  WO200177335-A2.
PD  18-OCT-2001.
PA  (INSP ) INST PASTEUR.
    Query Match                  6.5%;  Score 77.5;  DB 5;  Length 269;
    Best Local Similarity  22.0%;  Pred. No. 5.7;
RESULT 764
ID  ABG17374 standard; protein; 280 AA.
DE  Novel human diagnostic protein #17365.
PN  WO200175067-A2.
PD  11-OCT-2001.
PA  (HYSE-) HYSEQ INC.
    Query Match                  6.5%;  Score 77.5;  DB 4;  Length 280;
    Best Local Similarity  21.9%;  Pred. No. 6.1;
RESULT 765
ID  ABO00771 standard; protein; 280 AA.
DE  Polypeptide encoded by novel human contig #22.
PN  WO200303013-A2.
PD  20-MAR-2003.
PA  (HYSE-) HYSEQ INC.
    Query Match                  6.5%;  Score 77.5;  DB 6;  Length 280;
    Best Local Similarity  21.9%;  Pred. No. 6.1;
RESULT 766
ID  ABU48889 standard; protein; 327 AA.
DE  Protein encoded by Prokaryotic essential gene #34416.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
    Query Match                  6.5%;  Score 77.5;  DB 6;  Length 327;
    Best Local Similarity  24.8%;  Pred. No. 7.5;
RESULT 767
ID  AAW13576 standard; protein; 438 AA.
DE  Mouse Batten disease polypeptide CLN3 homologue.
PN  WO9708308-A1.
PD  06-MAR-1997.
PA  (GEHO ) GEN HOSPITAL CORP.
    (UYLE-) RIKSUNIV LEIDEN.
    Query Match                  6.5%;  Score 77.5;  DB 2;  Length 438;
    Best Local Similarity  27.6%;  Pred. No. 11;
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RESULT 768
ID   ADS42965 standard; protein; 491 AA.
DE   Bacterial polypeptide #21395.
PN   US20032323675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
PA   (MYRI-) MYRIAD GENETICS INC.
     Query Match       6.5%;  Score 77.5;  DB 8;  Pred. No. 13;  Length 491;
     Best Local Similarity  22.6%;

RESULT 769
ID   ADC42919 standard; protein; 892 AA.
DE   Variola smallpox virus A10L.
PN   WO2003017943-A2.
PD   06-MAR-2003.
PA   (MYRI-) MYRIAD GENETICS INC.
     Query Match       6.5%;  Score 77.5;  DB 7;  Pred. No. 30;  Length 892;
     Best Local Similarity  22.7%;

RESULT 770
ID   AEF63571 standard; protein; 930 AA.
DE   Ostreococcus tauri phospholipase 2 protein.
PN   WO200600809-A2.
PD   26-JAN-2006.
PA   (BADI ) BASF PLANT SCI GMBH.
     Query Match       6.5%;  Score 77.5;  DB 10;  Pred. No. 32;  Length 930;
     Best Local Similarity  19.7%;

RESULT 771
ID   AAR88413 standard; protein; 353 AA.
DE   High-affinity melatonin-1a receptor.
PN   WO9535320-A1.
PD   28-DEC-1995.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
     Query Match       6.5%;  Score 77.5;  DB 7;  Length 353;
     Best Local Similarity  19.7%;

RESULT 772
ID   AAW23958 standard; protein; 353 AA.
DE   Mouse melatonin 1a receptor.
PN   WO9803549-A1.
PD   29-JAN-1998.
PA   (GEHO ) GEN HOSPITAL CORP.
     Query Match       6.4%;  Score 77;  DB 2;  Pred. No. 9.6;  Length 353;
     Best Local Similarity  22.1%;

RESULT 773
ID   ABB07571 standard; protein; 353 AA.
DE   Mouse melatonin 1a (Mel1a) receptor.
PN   US6326526-B1.
PD   04-DEC-2001.
PA   (GEHO ) GEN HOSPITAL CORP.
     Query Match       6.4%;  Score 77;  DB 2;  Pred. No. 9.6;  Length 353;
     Best Local Similarity  22.1%;

RESULT 774
ID   ADO29553 standard; protein; 353 AA.
DE   Mouse GPCR MTNR1A, SEQ ID NO:655.
PN   WO200404000-A2.
PD   13-MAY-2004.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA   (GEHO ) GEN HOSPITAL CORP.
     Query Match       6.4%;  Score 77;  DB 5;  Pred. No. 9.6;  Length 353;
     Best Local Similarity  22.1%;

RESULT 775
ID   ADM25403 standard; protein; 383 AA.
DE   Hyperthermophile Methanopyrus kandleri protein #9.
PN   WO200307675-A2.
PD   18-SEP-2003.
PA   (PRIM-) PRIMAL INC.
     Query Match       6.4%;  Score 77;  DB 8;  Pred. No. 9.6;  Length 383;
     Best Local Similarity  22.1%;

RESULT 776
ID   ADQ95948 standard; protein; 490 AA.
DE   T cell activation associated protein #63.
PA   (FIDE-) FIDELITY SYSTEMS INC.
PA   (MAIY/) MALYKH A.
     Query Match       6.4%;  Score 77;  DB 7;  Pred. No. 11;  Length 490;
     Best Local Similarity  24.8%;


RESULT 777
ID   AAQ96002 standard; protein; 490 AA.
DE   T cell activation associated protein #90.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match       6.4%;  Score 77;  DB 8;  Pred. No. 15;  Length 490;
     Best Local Similarity  19.5%;

RESULT 778
ID   AAG42521 standard; protein; 648 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53040.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match       6.4%;  Score 77;  DB 3;  Pred. No. 15;  Length 648;
     Best Local Similarity  19.5%;

RESULT 779
ID   ABU16172 standard; protein; 650 AA.
DE   Protein encoded by Prokaryotic essential gene #1699.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match       6.4%;  Score 77;  DB 6;  Pred. No. 22;  Length 650;
     Best Local Similarity  27.5%;

RESULT 780
ID   ABM72713 standard; protein; 650 AA.
DE   Staphylococcus aureus protein #1953.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match       6.4%;  Score 77;  DB 6;  Pred. No. 22;  Length 650;
     Best Local Similarity  27.5%;

RESULT 781
ID   AAG42520 standard; protein; 690 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53039.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match       6.4%;  Score 77;  DB 3;  Pred. No. 24;  Length 690;
     Best Local Similarity  20.4%;

RESULT 782
ID   AAG42519 standard; protein; 728 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53038.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match       6.4%;  Score 77;  DB 3;  Pred. No. 26;  Length 728;
     Best Local Similarity  20.4%;

RESULT 783
ID   AAG32549 standard; protein; 805 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39287.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match       6.4%;  Score 77;  DB 3;  Pred. No. 30;  Length 805;
     Best Local Similarity  20.4%;

RESULT 784
ID   AAG32548 standard; protein; 847 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39286.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match       6.4%;  Score 77;  DB 3;  Pred. No. 32;  Length 847;
     Best Local Similarity  20.4%;

RESULT 785
ID   AAG32547 standard; protein; 991 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39285.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match       6.4%;  Score 77;  DB 3;  Pred. No. 40;  Length 991;
     Best Local Similarity  20.4%;

RESULT 786
ID   ABP52133 standard; protein; 1025 AA.
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DE   Plasmodium falciparummultidrug resistance protein SEQ ID NO:85.
PN   EP1217066-A1.
PD   26-JUN-2002.
PA   (UYGE-) UNIV GENT.

  Query Match   20.6%;  Score 77;  DB 5;  Length 1025;
  Best Local Similarity   20.6%;  Pred. No. 42;

RESULT 787
ID   AAG42381 standard; protein; 1047 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 52849.
PN   EP1033405-A2.
PD   06-SEP-2000.

  Query Match   20.4%;  Score 77;  DB 3;  Length 1047;
  Best Local Similarity   20.4%;  Pred. No. 43;

RESULT 788
ID   AAG42380 standard; protein; 1191 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 52848.
PN   EP1033405-A2.
PD   06-SEP-2000.

  Query Match   20.4%;  Score 77;  DB 3;  Length 1191;
  Best Local Similarity   20.4%;  Pred. No. 52;

RESULT 789
ID   AAG42379 standard; protein; 1202 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 52847.
PN   EP1033405-A2.
PD   06-SEP-2000.

  Query Match   20.4%;  Score 77;  DB 3;  Length 1202;
  Best Local Similarity   20.4%;  Pred. No. 52;

RESULT 790
ID   AAR29527 standard; protein; 2510 AA.
DE   HCV antigen T7N1-30.
PN   EP518313-A2.
PD   16-DEC-1992.
PA   (MITU ) MITSUBISHI KASEI CORP.

  Query Match   22.5%;  Score 77;  DB 2;  Length 2510;
  Best Local Similarity   22.5%;  Pred. No. 1.5e+02;

RESULT 791
ID   ADX40818 standard; protein; 3010 AA.
DE   HCV polymerase protein #41.
PN   WO2005012502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.

  Query Match   22.5%;  Score 77;  DB 9;  Length 3010;
  Best Local Similarity   22.5%;  Pred. No. 1.9e+02;

RESULT 792
ID   ADX40816 standard; protein; 3010 AA.
DE   HCV polymerase protein #39.
PN   WO2005012502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.

  Query Match   22.5%;  Score 77;  DB 9;  Length 3010;
  Best Local Similarity   22.5%;  Pred. No. 1.9e+02;

RESULT 793
ID   ADT56855 standard; protein; 195 AA.
DE   Plant polypeptide, SEQ ID 6932.
PN   US2004216190-A1.
PD   28-OCT-2004.
PA   (KOVA/) KOVALIC D K.

  Query Match   25.8%;  Score 76.5;  DB 8;  Length 195;
  Best Local Similarity   25.8%;  Pred. No. 4.8;

RESULT 794
ID   ADF74966 standard; protein; 249 AA.
DE   Human 164-1h protein (SeqID 25).
PN   WO2003097686-A1.
PD   27-NOV-2003.
PA   (TAKE ) TAKEDA CHEM IND LTD.

  Query Match   23.3%;  Score 76.5;  DB 8;  Length 249;
  Best Local Similarity   23.3%;  Pred. No. 6.7;

RESULT 795
ID   ADC01137 standard; protein; 278 AA.
DE   Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1181.
PN   JP2002355074-A.
PD   10-DEC-2002.
PA   (UYTS-) UNIV TSUKUBA.

  Query Match   28.5%;  Score 76.5;  DB 7;  Length 278;
  Best Local Similarity   28.5%;  Pred. No. 7.9;

RESULT 796
ID   ABO65827 standard; protein; 435 AA.
DE   Klebsiella pneumoniae polypeptide seqid 12344.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.

  Query Match   21.8%;  Score 76.5;  DB 7;  Length 435;
  Best Local Similarity   21.8%;  Pred. No. 15;

RESULT 797
ID   ADF74969 standard; protein; 481 AA.
DE   Human 164-1b protein (seqid 28).
PN   WO2003097686-A1.
PD   27-NOV-2003.
PA   (TAKE ) TAKEDA CHEM IND LTD.

  Query Match   21.8%;  Score 76.5;  DB 7;  Length 481;
  Best Local Similarity   21.8%;  Pred. No. 15;

RESULT 798
ID   AAR90765 standard; protein; 494 AA.
DE   Human K+ channel 2 mature protein.
PN   WO9603415-A1.
PD   08-FEB-1996.
PA   (HUMA-) HUMAN GENOME SCI INC.

  Query Match   23.3%;  Score 76.5;  DB 8;  Length 494;
  Best Local Similarity   23.3%;  Pred. No. 17;

RESULT 799
ID   AAW42996 standard; protein; 494 AA.
DE   Putative mature potassium channel 2 protein.
PN   US5710019-A.
PD   20-JAN-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.

  Query Match   21.3%;  Score 76.5;  DB 2;  Length 494;
  Best Local Similarity   21.3%;  Pred. No. 17;

RESULT 800
ID   ABP58356 standard; protein; 494 AA.
DE   Human potassium channel subunit Kv5.1.
PN   WO200296944-A2.
PD   05-DEC-2002.
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

  Query Match   21.3%;  Score 76.5;  DB 6;  Length 494;
  Best Local Similarity   21.3%;  Pred. No. 17;

RESULT 801
ID   ADC99155 standard; protein; 494 AA.
DE   Human mature K+ channel 2 protein.
PN   US2003092895-A1.
PD   15-MAY-2003.
PA   (LIYY/) LI Y.
PA   (ADAM/) ADAMS M D.
PA   (WHIT/) WHITE O R.

  Query Match   21.3%;  Score 76.5;  DB 7;  Length 494;
  Best Local Similarity   21.3%;  Pred. No. 17;

RESULT 802
ID   AAW20085 standard; protein; 509 AA.
DE   Helicobacter pylori cytoplasmic protein, 10009666.aa.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (ASTR ) ASTRA AB.

  Query Match   19.2%;  Score 76.5;  DB 2;  Length 509;
  Best Local Similarity   19.2%;  Pred. No. 18;

RESULT 803
ID   ADQ07984 standard; protein; 526 AA.
DE   Human hypothetical protein FLJ20371-encoding cDNA.
PN   WO2004061123-A2.
PD   22-JUL-2004.
PA   (EXEL-) EXELIXIS INC.

  Query Match   15.7%;  Score 76.5;  DB 8;  Length 526;
  Best Local Similarity   15.7%;  Pred. No. 19;

RESULT 804
ID   ADP25065 standard; protein; 526 AA.
DE   PRO polypeptide SEQ ID NO:2243.
PN   WO2004041170-A2.
PD   21-MAY-2004.

PA   (GETH ) GENENTECH INC.
Query Match 6.4%;
Best Local Similarity 15.7%; Score 76.5; DB 8; Length 526; Pred. No. 19;

RESULT 805
ID   ADU06638 standard; protein; 526 AA.
DE   Novel bronchial cancer-associated human protein SeqID864.
PN   DE10316701-A1.
PD   04-NOV-2004.
PA   (HINZ/) HINZMANN B.
PA   (HERM/) HERMANN K.
PA   (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 6.4%;
Best Local Similarity 15.7%; Score 76.5; DB 8; Length 526; Pred. No. 19;

RESULT 806
ID   ADB63857 standard; protein; 555 AA.
DE   Human protein encoded by clone ASTR02005430.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%;
Best Local Similarity 23.3%; Score 76.5; DB 7; Length 555; Pred. No. 21;

RESULT 807
ID   ABB08159 standard; protein; 570 AA.
DE   Human cytoskeleton-associated protein (CSAP)-3 (ID: 7091536CD1).
PN   WO200242330-A2.
PD   30-MAY-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%;
Best Local Similarity 23.3%; Score 76.5; DB 5; Length 570; Pred. No. 21;

RESULT 808
ID   AAW20918 standard; protein; 593 AA.
DE   H. pylori transporter protein, 14gp12o15orf14.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (ASTR ) ASTRA AB.
Query Match 6.4%;
Best Local Similarity 19.2%; Score 76.5; DB 2; Length 593; Pred. No. 22;

RESULT 809
ID   ADN46225 standard; protein; 615 AA.
DE   Thermococcus kodakaraensis KOD1 protein sequence SeqID103.
PN   WO20040222736-A1.
PD   18-MAR-2004.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.4%;
Best Local Similarity 22.6%; Score 76.5; DB 8; Length 615; Pred. No. 24;

RESULT 810
ID   ADN21126 standard; protein; 2539 AA.
DE   Bacterial polypeptide #3779.
PN   US20032233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match 6.4%;
Best Local Similarity 22.1%; Score 76.5; DB 8; Length 2539; Pred. No. 1.7e+02;

RESULT 811
ID   ADH8107 standard; protein; 195 AA.
DE   Bacterial polypeptide #2587.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
Query Match 6.4%;
Best Local Similarity 25.9%; Score 76; DB 7; Length 195; Pred. No. 5.5;

RESULT 812
ID   AAG09592 standard; protein; 274 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 7586.
PN   EP1033405-A2.
PD   06-SEP-2000.
Query Match 6.4%;
Best Local Similarity; Score 76; DB 3; Length 274; Pred. No. 1.7e+02;

Best Local Similarity 26.7%; Score 76; DB 3; Length 287; Pred. No. 8.8;

RESULT 813
ID   AAG09591 standard; protein; 287 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 7585.
PN   EP1033405-A2.
PD   06-SEP-2000.
Query Match 6.4%;
Best Local Similarity 26.7%; Score 76; DB 3; Length 287; Pred. No. 9.4;

RESULT 814
ID   ADQ96244 standard; protein; 366 AA.
DE   T cell activation associated protein #211.
PN   WO20040588805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 6.4%;
Best Local Similarity 22.0%; Score 76; DB 8; Length 366; Pred. No. 13;

RESULT 815
ID   ADQ96246 standard; protein; 366 AA.
DE   T cell activation associated protein #212.
PN   WO20040588805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 6.4%;
Best Local Similarity 22.0%; Score 76; DB 8; Length 366; Pred. No. 18;

RESULT 816
ID   ABB89424 standard; protein; 456 AA.
DE   Human colon cancer antigen protein sequence SEQ ID NO:940.
PN   WO200055351-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%;
Best Local Similarity 22.0%; Score 76; DB 5; Length 456; Pred. No. 18;

RESULT 817
ID   AAB53400 standard; protein; 557 AA.
DE   Human colon cancer antigen protein SEQ ID NO 1800.
PN   WO200190104-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%;
Best Local Similarity 22.0%; Score 76; DB 5; Length 557; Pred. No. 24;

RESULT 818
ID   AAY44945 standard; protein; 593 AA.
DE   Wheat sulphate permease-2.
PN   WO20000004154-A2.
PD   27-JAN-2000.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
Query Match 6.4%;
Best Local Similarity 22.0%; Score 76; DB 3; Length 593; Pred. No. 24;

RESULT 819
ID   ADN22849 standard; protein; 1402 AA.
DE   Bacterial polypeptide #5502.
PN   US20032233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match 6.4%;
Best Local Similarity 21.4%; Score 76; DB 8; Length 1402; Pred. No. 26;

RESULT 820
ID   AEF10990 standard; protein; 1783 AA.
DE   C. elegans VDCC alpha 1 subunit, Cav2.1.
PN   US20052848489-A1.
PD   29-DEC-2005.
PA   (HIRS/) HIRSCH J A.
Query Match 6.4%;
Best Local Similarity 20.2%; Score 76; DB 10; Length 1783; Pred. No. 85;

RESULT 821
ID   ADN23383 standard; protein; 1917 AA.
DE   Bacterial polypeptide #6036.
PN   US20032233675-A1.
PD   18-DEC-2003.
Query Match 6.4%;
Best Local Similarity 18.5%; Score 76; DB 8; Length 1917; Pred. No. 1.2e+02;

PA  (CAOY/) CAO Y.
PA  (HINK/) HINKLE G J.
PA  (SLAT/) SLATER S C.
PA  (CHEN/) CHEN X.
PA  (GOLD/) GOLDMAN B S.
PA  (EPIM-) EPIMMUNE INC.
    Query Match
    Best Local Similarity   18.5%;  Score 76;  Pred. No. 1.3e+02;  DB 8;  Length 1917;
RESULT 823
ID  ADX40794 standard; protein; 3010 AA.
DE  HCV polymerase protein #17.
PN  WO200501250A-A2.
PD  10-FEB-2005.
PA  (EPIM-) EPIMMUNE INC.
    Query Match
    Best Local Similarity   25.4%;  Score 76;  Pred. No. 2.5e+02;  DB 9;  Length 3010;
RESULT 824
ID  ADX40791 standard; protein; 3010 AA.
DE  HCV polymerase protein #14.
PN  WO200501250A-A2.
PD  10-FEB-2005.
PA  (EPIM-) EPIMMUNE INC.
    Query Match
    Best Local Similarity   25.4%;  Score 76;  Pred. No. 2.5e+02;  DB 9;  Length 3010;
RESULT 825
ID  ADX40792 standard; protein; 3010 AA.
DE  HCV polymerase protein #15.
PN  WO200501250A-A2.
PD  10-FEB-2005.
PA  (EPIM-) EPIMMUNE INC.
    Query Match
    Best Local Similarity   26.9%;  Score 76;  Pred. No. 2.5e+02;  DB 9;  Length 3010;
RESULT 826
ID  ABB63150 standard; protein; 228 AA.
DE  Drosophila melanogaster polypeptide SEQ ID No 16242.
PN  WO200171042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match
    Best Local Similarity   21.8%;  Score 76;  Pred. No. 7.8;  DB 4;  Length 228;
RESULT 827
ID  ADK46633 standard; protein; 263 AA.
DE  Streptococcus pneumoniae protein, Seq ID No 3148.
PN  US669703-B1.
PD  02-MAR-2004.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match
    Best Local Similarity   18.0%;  Score 75.5;  Pred. No. 9.5;  DB 8;  Length 263;
RESULT 828
ID  ADM92206 standard; protein; 263 AA.
DE  S pneumoniae antigenic protein sequence SeqID403.
PN  WO200402060-A2.
PD  11-MAR-2004.
PA  (TUFT ) UNIV TUFTS.
    Query Match
    Best Local Similarity   18.0%;  Score 75.5;  Pred. No. 9.5;  DB 3;  Length 263;
RESULT 829
ID  AAY81619 standard; protein; 264 AA.
DE  Streptococcus pneumoniae type 4 protein sequence #119.
PN  WO200006737-A2.
PD  10-FEB-2000.
PA  (MICR-) MICROBIAL TECHNICS LTD.
    Query Match
    Best Local Similarity   18.0%;  Score 75.5;  Pred. No. 9.5;  DB 8;  Length 264;
RESULT 829
ID  ADR96242 standard; protein; 264 AA.
DE  Novel S. pneumoniae protein sequence, SEQ ID 4877.
PN  US5800744-B1.
PD  05-OCT-2004.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match
    Best Local Similarity   18.0%;  Score 75.5;  Pred. No. 9.6;  DB 3;  Length 264;
RESULT 830
ID  AEA60112 standard; protein; 264 AA.
DE  Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:4877.
PN  US2005136404-A1.
PD  23-JUN-2005.
PA  (DOUC/) DOUCETTE-STAMM L A.
PA  (BUSH/) BUSH D.
    Query Match
    Best Local Similarity   18.0%;  Score 75.5;  Pred. No. 9.6;  DB 9;  Length 264;
RESULT 831
ID  ABU02182 standard; protein; 276 AA.
DE  S. pneumoniae type 4 strain protein from coding region #1759.
PN  WO200277021-A2.
PD  03-OCT-2002.
PA  (CHIR-) CHIRON SPA.
PA  (GENO-) INST GENOMIC RES.
    Query Match
    Best Local Similarity   18.0%;  Score 75.5;  Pred. No. 10;  DB 6;  Length 276;
RESULT 832
ID  ABG93285 standard; protein; 342 AA.
DE  C. albicans BAX-associated protein fragment SEQ ID 528.
PN  WO200264766-A2.
PD  22-AUG-2002.
PA  (JANC ) JANSSEN PHARM NV.
    Query Match
    Best Local Similarity   21.9%;  Score 75.5;  Pred. No. 14;  DB 5;  Length 342;
RESULT 833
ID  AAB15936 standard; protein; 352 AA.
DE  E. coli proliferation associated protein sequence SEQ ID NO:293.
PN  WO200044906-A2.
PD  03-AUG-2000.
PA  (GENO-) JANSSEN PHARM.
    Query Match
    Best Local Similarity   31.7%;  Score 75.5;  Pred. No. 14;  DB 3;  Length 352;
RESULT 834
ID  ADH51470 standard; protein; 363 AA.
DE  Rat MT1 receptor amino acid sequence #SEQ ID 2.
PN  FR2835847-A1.
PD  15-AUG-2003.
PA  (SERV-) LES LAB SERVIER SA.
    Query Match
    Best Local Similarity   23.5%;  Score 75.5;  Pred. No. 14;  DB 7;  Length 363;
RESULT 835
ID  AAU03851 standard; protein; 397 AA.
DE  G protein-coupled receptor-like (GPCR-like) receptor protein #23.
PN  WO200138533-A2.
PD  31-MAY-2001.
PA  (PHA ) PHARMACIA & UPJOHN.
    Query Match
    Best Local Similarity   6.3%;  Score 75.5;  Pred. No. 15;  DB 4;  Length 397;
RESULT 836
ID  ADU92092 standard; protein; 415 AA.
DE  Escherichia coli TnaB protein.
PN  EP1484410-A1.
PD  08-DEC-2004.
PA  (AJIN ) AJINOMOTO KK.
    Query Match
    Best Local Similarity   19.1%;  Score 75.5;  Pred. No. 17;  DB 4;  Length 415;
RESULT 837
ID  AEB41698 standard; protein; 430 AA.
DE  L. pneumophila protein SEQ ID NO 6030.
PN  WO200504964-A2.
PD  02-JUN-2005.
PA  (INSP ) INST PASTEUR.
PA  (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA  (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA  (CNRS ) CNRS CENT NAT RECH SCI.
    Query Match
    Best Local Similarity   25.5%;  Score 75.5;  Pred. No. 18;  DB 9;  Length 430;
RESULT 838
ID  AAU03852 standard; protein; 433 AA.
DE  G protein-coupled receptor-like (GPCR-like) receptor protein #24.
PN  WO200138533-A2.
PD  31-MAY-2001.
PA  (PHAA ) PHARMACIA & UPJOHN.

Query Match
Best Local Similarity   19.1%;   Score 75.5;   DB 4;   Pred. No. 19;   Length 433;

RESULT 839
ID   AEB38437 standard; protein; 436 AA.
DE   L. pneumophila protein SEQ ID NO 2769.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP )  INST PASTEUR.
PA   (INRM )  INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-)  UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS )  CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity   25.5%;   Score 75.5;   DB 9;   Pred. No. 19;   Length 436;

RESULT 840
ID   ADS24239 standard; protein; 463 AA.
DE   Bacterial polypeptide #13272.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/)  CAO Y.
PA   (HINK/)  HINKLE G J.
PA   (SLAT/)  SLATER S C.
PA   (CHEN/)  CHEN X.
PA   (GOLD/)  GOLDMAN B S.
Query Match
Best Local Similarity   21.4%;   Score 75.5;   DB 8;   Pred. No. 19;   Length 463;

RESULT 841
ID   ADO29507 standard; protein; 471 AA.
DE   Mouse GPCR HTR2A, SEQ ID NO:609.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-)  PRIMAL INC.
Query Match
Best Local Similarity   21.0%;   Score 75.5;   DB 8;   Pred. No. 21;   Length 471;

RESULT 842
ID   AAU03820 standard; protein; 499 AA.
DE   G protein-coupled receptor-like (GPCR-like) receptor protein #19.
PN   WO200138533-A2.
PD   31-MAY-2001.
PA   (PHAA )  PHARMACIA & UPJOHN.
Query Match
Best Local Similarity   19.1%;   Score 75.5;   DB 4;   Pred. No. 21;   Length 499;

RESULT 843
ID   ADM72132 standard; protein; 392 AA.
DE   Human NTRAN polypeptide (clone ID 752455CD1).
PN   WO2004022705-A2.
PD   18-MAR-2003.
PA   (INCY-)  INCYTE CORP.
Query Match
Best Local Similarity   21.0%;   Score 75.5;   DB 8;   Pred. No. 23;   Length 392;

RESULT 844
ID   ABM90212 standard; protein; 404 AA.
DE   Rice abiotic stress responsive polypeptide SEQ ID NO:8934.
PN   WO2003008540-A2.
PD   30-JAN-2003.
PA   (SYGN )  SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity   15.6%;   Score 75;   DB 7;   Pred. No. 20;   Length 404;

RESULT 845
ID   AEB39222 standard; protein; 418 AA.
DE   L. pneumophila protein SEQ ID NO 3554.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP )  INST PASTEUR.
PA   (INRM )  INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-)  UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS )  CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity   20.7%;   Score 75;   DB 9;   Pred. No. 21;   Length 418;

RESULT 846
ID   AEB35772 standard; protein; 437 AA.
DE   L. pneumophila protein SEQ ID NO 104.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP )  INST PASTEUR.
PA   (INRM )  INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-)  UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS )  CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity   20.7%;   Score 75;   DB 9;   Pred. No. 22;   Length 437;

RESULT 847
ID   AAU45917 standard; protein; 445 AA.
DE   Propionibacterium acnes immunogenic protein #6813.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-)  CORIXA CORP.
Query Match
Best Local Similarity   24.8%;   Score 75;   DB 9;   Pred. No. 23;   Length 445;

RESULT 848
ID   ABM42436 standard; protein; 445 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #7112.
PN   WO2003033515-A1.
PD   24-APR-2003.
PA   (CORI-)  CORIXA CORP.
Query Match
Best Local Similarity   24.8%;   Score 75;   DB 4;   Pred. No. 23;   Length 445;

RESULT 849
ID   ABM87563 standard; protein; 452 AA.
DE   Rice abiotic stress responsive polypeptide SEQ ID NO:5809.
PN   WO2003008540-A2.
PD   30-JAN-2003.
PA   (SYGN )  SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity   15.6%;   Score 75;   DB 7;   Pred. No. 23;   Length 452;

RESULT 850
ID   ADA34178 standard; protein; 467 AA.
DE   Acinetobacter baumannii protein #1339.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-)  GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity   21.0%;   Score 75;   DB 6;   Pred. No. 24;   Length 467;

RESULT 851
ID   ADR14597 standard; protein; 473 AA.
DE   Human NF-kappaB pathway-associated protein SeqID598.
PN   WO2004065577-A2.
PD   05-AUG-2004.
PA   (BRIM )  BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity   23.1%;   Score 75;   DB 8;   Pred. No. 25;   Length 473;

RESULT 852
ID   ADP99138 standard; protein; 480 AA.
DE   Human transporter and ion channel (TRICH) protein - SEQ ID 3.
PN   WO2004048599-A2.
PD   10-JUN-2004.
PA   (INCY-)  INCYTE CORP.
Query Match
Best Local Similarity   21.0%;   Score 75;   DB 8;   Pred. No. 25;   Length 480;

RESULT 853
ID   ADH86490 standard; protein; 549 AA.
DE   Enterococcus faecalis polypeptide #970.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/)  DOUCETTE-STAMM L A.
PA   (BUSH/)  BUSH D.
Query Match
Best Local Similarity   21.0%;   Score 75;   DB 7;   Pred. No. 25;   Length 549;

RESULT 854
ID   ADX80121 standard; protein; 635 AA.
DE   Plant full length insert polypeptide seqid 49487.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIU7/)  LIU J.
PA   (ZHOU/)  ZHOU Y.
PA   (KOVA/)  KOVALIC D K.
PA   (SCRE/)  SCREEN S B.
PA   (TABA/)  TABASKA J E.
Query Match
Best Local Similarity   18.7%;   Score 75;   DB 7;   Pred. No. 30;   Length 635;

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PA  (CAOY/) CAO Y.
    Query Match                              Pred. No. 37;
    Best Local Similarity  25.3%;  Score 75;  DB 8;  Length 635;

RESULT 855
ID  PAR54066 standard; protein; 1051 AA.
DE  Non-A, non-B hepatitis virus gene #4 product.
PN  JP06141870-A.
PD  24-MAY-1994.
PA  (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA  (SANW ) SANWA KAGAKU KENKYUSHO CO.
PA  (TOFU ) TONEN CORP.
    Query Match                              Pred. No. 75;
    Best Local Similarity  23.4%;  Score 75;  DB 2;  Length 1051;

RESULT 856
ID  AAR98361 standard; protein; 1051 AA.
DE  5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).
PN  JP07133291-A.
PD  23-MAY-1995.
PA  (TOFU ) TONEN CORP.
    Query Match                              Pred. No. 75;
    Best Local Similarity  23.4%;  Score 75;  DB 2;  Length 1051;

RESULT 857
ID  ADB64712 standard; protein; 1131 AA.
DE  Human protein encoded by clone NT2NE20072270.
PN  EP1308459-A2.
PD  07-MAY-2003.
PA  (HELI-) HELIX RES INST.
PA  (REAS-) RES ASSOC BIOTECHNOLOGY.
    Query Match                              Pred. No. 83;
    Best Local Similarity  23.9%;  Score 75;  DB 7;  Length 1131;

RESULT 858
ID  ABB64494 standard; protein; 2248 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 20274.
PN  WO200171042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
    Query Match                              Pred. No. 2.1e+02;
    Best Local Similarity  22.9%;  Score 75;  DB 4;  Length 2248;

RESULT 859
ID  ADG20763 standard; protein; 2248 AA.
DE  Drosophila melanogaster rutabaga protein SEQ ID NO:2.
PN  WO2003103704-A2.
PD  18-DEC-2003.
PA  (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
    Query Match                              Pred. No. 2.1e+02;
    Best Local Similarity  22.9%;  Score 75;  DB 8;  Length 2248;

RESULT 860
ID  ADQ89656 standard; protein; 2248 AA.
DE  Antagonist of cell cycle progression polypeptide #43.
PN  WO2004063362-A2.
PD  29-JUL-2004.
PA  (CYCL-) CYCLACEL LTD.
    Query Match                              Pred. No. 2.1e+02;
    Best Local Similarity  22.9%;  Score 75;  DB 8;  Length 2248;

RESULT 861
ID  ADX40796 standard; protein; 3010 AA.
DE  HCV polymerase protein #19.
PN  WO2005013502-A2.
PD  10-FEB-2005.
PA  (EPIM-) EPIMMUNE INC.
    Query Match                              Pred. No. 3.2e+02;
    Best Local Similarity  22.9%;  Score 75;  DB 9;  Length 3010;

RESULT 862
ID  AAB66797 standard; protein; 200 AA.
DE  Porcine reproductive and respiratory syndrome virus ORF #5 protein.
PN  WO200102858-A1.
PD  11-JAN-2001.
PA  (MOLE-) INST MOLECULAR AGROBIOLOGY.
    Query Match                              Pred. No. 8.6;
    Best Local Similarity  23.8%;  Score 74.5;  DB 4;  Length 200;

RESULT 863
ID  ADF74954 standard; protein; 256 AA.
DE  Rat 164-1h protein (SeqID 13).
PN  WO200309768-A1.
PD  27-NOV-2003.
PA  (TAKE ) TAKEDA CHEM IND LTD.
    Query Match                              Pred. No. 12;
    Best Local Similarity  23.3%;  Score 74.5;  DB 8;  Length 256;

RESULT 864
ID  AAR53748 standard; protein; 355 AA.
DE  Seven transmembrane receptor (V28).
PN  WO9412635-A2.
PD  09-JUN-1994.
PA  (ICOS-) ICOS CORP.
    Query Match                              Pred. No. 19;
    Best Local Similarity  25.8%;  Score 74.5;  DB 2;  Length 355;

RESULT 865
ID  AAW48722 standard; protein; 355 AA.
DE  Human V28 seven transmembrane receptor.
PN  US5759804-A.
PD  02-JUN-1998.
PA  (ICOS-) ICOS CORP.
    Query Match                              Pred. No. 19;
    Best Local Similarity  25.8%;  Score 74.5;  DB 2;  Length 355;

RESULT 866
ID  AAY90677 standard; protein; 355 AA.
DE  Human mutant G protein-coupled receptor V28 (I230K).
PN  WO200022129-A1.
PD  20-APR-2000.
PA  (AREN-) ARENA PHARM INC.
    Query Match                              Pred. No. 19;
    Best Local Similarity  25.8%;  Score 74.5;  DB 3;  Length 355;

RESULT 867
ID  AAY90642 standard; protein; 355 AA.
DE  Human G protein-coupled receptor V28.
PN  WO200022129-A1.
PD  20-APR-2000.
PA  (AREN-) ARENA PHARM INC.
    Query Match                              Pred. No. 19;
    Best Local Similarity  25.8%;  Score 74.5;  DB 3;  Length 355;

RESULT 868
ID  AAB21693 standard; protein; 355 AA.
DE  Human 7TM receptor V28 cDNA clone protein #2.
PN  US6107475-A.
PD  22-AUG-2000.
PA  (ICOS-) ICOS CORP.
    Query Match                              Pred. No. 19;
    Best Local Similarity  25.8%;  Score 74.5;  DB 3;  Length 355;

RESULT 869
ID  AAB21692 standard; protein; 355 AA.
DE  Human 7TM receptor V28 cDNA clone protein #1.
PN  US6107475-A.
PD  22-AUG-2000.
PA  (ICOS-) ICOS CORP.
    Query Match                              Pred. No. 19;
    Best Local Similarity  25.8%;  Score 74.5;  DB 3;  Length 355;

RESULT 870
ID  AAG80126 standard; protein; 355 AA.
DE  Human CX3CR1 protein.
PN  WO200172830-A2.
PD  04-OCT-2001.
PA  (FORS/) FORSSMANN U.
    Query Match                              Pred. No. 19;
    Best Local Similarity  25.8%;  Score 74.5;  DB 4;  Length 355;

RESULT 871
ID  AAB82786 standard; protein; 355 AA.
DE  Human CX3C chemokine receptor 1.
PN  WO200160406-A1.
PD  23-AUG-2001.
PA  (MILL-) MILLENNIUM PHARM INC.
PA  (NOUN ) UNIV NORTHWESTERN.
    Query Match                              Pred. No. 19;
    Best Local Similarity  25.8%;  Score 74.5;  DB 4;  Length 355;

RESULT 872
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ID   AAU91235 standard; protein; 355 AA.
DE   Human 7 transmembrane domain receptor V28 #2.
PN   US6348574-B1.
PD   19-FEB-2002.
PA   (ICOS-) ICOS CORP.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 5;   Length 355;
RESULT 873

ID   AAU91234 standard; protein; 355 AA.
DE   Human 7 transmembrane domain receptor V28 #1.
PN   US6348574-B1.
PD   19-FEB-2002.
PA   (ICOS-) ICOS CORP.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 5;   Length 355;
RESULT 874

ID   AAU84327 standard; protein; 355 AA.
DE   Protein CX3CR1 differentially expressed in breast cancer tissue.
PN   WO200210436-A2.
PD   07-FEB-2002.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
     (BAAK/) BAAK J.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 5;   Length 355;
RESULT 875

ID   ABR58524 standard; protein; 355 AA.
DE   Human chemokine (C-X3-C) receptor 1 protein.
PN   WO200302138-A2.
PD   27-MAR-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 6;   Length 355;
RESULT 876

ID   AAO29513 standard; protein; 355 AA.
DE   Human fractalkine receptor (313) protein.
PN   WO200303475-A2.
PD   15-MAY-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 6;   Length 355;
RESULT 877

ID   ABP97732 standard; protein; 355 AA.
DE   Amino acid sequence of human chemokine receptor CX3CR1.
PN   WO200314153-A2.
PD   20-FEB-2003.
PA   (TOPI-) TOPIGEN PHARM INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 6;   Length 355;
RESULT 878

ID   ABP81882 standard; protein; 355 AA.
DE   Human CX3C chemokine fractalkine receptor 1 protein SEQ ID NO:249.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 6;   Length 355;
RESULT 879

ID   ADC22751 standard; protein; 355 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #74.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 7;   Length 355;
RESULT 880

ID   ADC22649 standard; protein; 355 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #34.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 7;   Length 355;
RESULT 881

ID   ADH14224 standard; protein; 355 AA.
DE   Mutated human serotonin V28.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
     (BEHA/) BEHAN D P.
     (CHAL/) CHALMERS D T.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 7;   Length 355;
RESULT 882

ID   ADH14122 standard; protein; 355 AA.
DE   Human serotonin V28.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
     (BEHA/) BEHAN D P.
     (CHAL/) CHALMERS D T.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 7;   Length 355;
RESULT 883

ID   ADH10680 standard; protein; 355 AA.
DE   Human CX3CR1 polypeptide.
PN   WO200310484-A1.
PD   18-DEC-2003.
PA   (META-) METABOLEX INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 8;   Length 355;
RESULT 884

ID   ADO22269 standard; protein; 355 AA.
DE   Human GPCR CX3CR1, SEQ ID NO:370.
PN   WO200404000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 8;   Length 355;
RESULT 885

ID   ADQ18141 standard; protein; 355 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 958.
PN   WO200404938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 8;   Length 355;
RESULT 886

ID   ADP56020 standard; protein; 355 AA.
DE   Human PRO protein sequence SEQ ID NO:1996.
PN   WO200403956-A2.
PD   13-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 8;   Length 355;
RESULT 887

ID   ADP54585 standard; protein; 355 AA.
DE   Human PRO protein sequence SEQ ID NO:561.
PN   WO200403956-A2.
PD   13-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 8;   Length 355;
RESULT 888

ID   ADP23931 standard; protein; 355 AA.
DE   PRO polypeptide SEQ ID NO:1109.
PN   WO200404170-A2.
PD   21-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   25.8%;   Score 74.5;   DB 8;   Length 355;
RESULT 889

ID   ADQ39421 standard; protein; 355 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1084.
PN   WO200405052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.

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Query Match    Best Local Similarity 25.8%;   Score 74.5;   Pred. No. 19;   DB 8;   Length 355;

RESULT 890
ID   ADY15644 standard; protein; 355 AA.
PN   WO2005016962-A2.
DE   PRO polypeptide SEQ ID NO 1450.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.

Query Match    Best Local Similarity 25.8%;   Score 74.5;   Pred. No. 19;   DB 9;   Length 355;

RESULT 891
ID   AED67635 standard; protein; 355 AA.
DE   Human CX3C chemokine receptor 1 (CX3CR1).
PN   WO2005103684-A2.
PD   03-NOV-2005.
PA   (FARB ) BAYER HEALTHCARE AG.

Query Match    Best Local Similarity 25.8%;   Score 74.5;   Pred. No. 19;   DB 9;   Length 362;

RESULT 892
ID   ADQ39422 standard; protein; 362 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1085.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.

Query Match    Best Local Similarity 21.0%;   Score 74.5;   Pred. No. 28;   DB 2;   Length 471;

RESULT 893
ID   AAW77109 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor C322K mutant.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.

Query Match    Best Local Similarity 21.0%;   Score 74.5;   Pred. No. 28;   DB 2;   Length 471;

RESULT 894
ID   AAW77111 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor C322E mutant.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.

Query Match    Best Local Similarity 21.0%;   Score 74.5;   Pred. No. 28;   DB 2;   Length 471;

RESULT 895
ID   AAW77110 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor C322R mutant.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.

Query Match    Best Local Similarity 21.0%;   Score 74.5;   Pred. No. 28;   DB 2;   Length 471;

RESULT 896
ID   AAW77104 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.

Query Match    Best Local Similarity 21.0%;   Score 74.5;   Pred. No. 28;   DB 5;   Length 471;

RESULT 897
ID   ABB07980 standard; protein; 471 AA.
DE   Rat 5-HT2 receptor sequence.
PN   US6383762-B1.
PD   07-MAY-2002.
PA   (SYNA-) SYNAPTIC PHARM CORP.

Query Match    Best Local Similarity 21.0%;   Score 74.5;   Pred. No. 28;   DB 8;   Length 481;

RESULT 898
ID   ADF74971 standard; protein; 481 AA.
DE   Rat 164-1b protein (SeqID 30).
PN   WO2003097696-A1.
PD   27-NOV-2003.
PA   (TAKE ) TAKEDA CHEM IND LTD.

Query Match    Best Local Similarity 23.3%;   Score 74.5;   Pred. No. 29;   DB 8;   Length 562;

RESULT 899
ID   AAM93692 standard; protein; 562 AA.
DE   Human polypeptide, SEQ ID NO: 3602.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.

Query Match    Best Local Similarity 23.1%;   Score 74.5;   Pred. No. 36;   DB 4;   Length 562;

RESULT 900
ID   ADJ31569 standard; protein; 562 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3602.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match    Best Local Similarity 23.1%;   Score 74.5;   Pred. No. 36;   DB 8;   Length 587;

RESULT 901
ID   ADQ96118 standard; protein; 587 AA.
DE   T cell activation associated gene protein #158.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.

Query Match    Best Local Similarity 23.1%;   Score 74.5;   Pred. No. 36;   DB 8;   Length 562;

RESULT 902
ID   ADR86160 standard; protein; 562 AA.
DE   Aspergillus fumigatus essential gene protein #210.
PN   WO2004067709-A2.
PD   12-AUG-2004.
PA   (ELIT-) ELITRA PHARM INC.

Query Match    Best Local Similarity 18.2%;   Score 74.5;   Pred. No. 38;   DB 8;   Length 597;

RESULT 903
ID   ABB62948 standard; protein; 597 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 15636.
PN   WO2001171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.

Query Match    Best Local Similarity 27.2%;   Score 74.5;   Pred. No. 39;   DB 4;   Length 661;

RESULT 904
ID   ADX66440 standard; protein; 661 AA.
DE   Plant full length insert polypeptide seqid 37283.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.

Query Match    Best Local Similarity 20.4%;   Score 74.5;   Pred. No. 45;   DB 8;   Length 940;

RESULT 905
ID   ADA36878 standard; protein; 940 AA.
DE   Acinetobacter baumannii protein #4039.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.

Query Match    Best Local Similarity 21.1%;   Score 74.5;   Pred. No. 73;   DB 6;   Length 1808;

RESULT 906
ID   ABB92731 standard; protein; 1808 AA.
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DE   Herbicidally active polypeptide SEQ ID NO 1942.
PN   WO020210210-A2.
PD   07-FEB-2002.
PA   (FARB) BAYER AG.

Query Match             6.2%;
Best Local Similarity  17.3%;  Score 74.5;  DB 5;  Pred. No. 1.8e+02;  Length 1808;

RESULT 907
ID   AAE20477 standard; protein; 3010 AA.
DE   HCV-S1 full-length polyprotein.
PN   WO020208447-A2.
PD   31-JAN-2002.
PA   (MOLE-) INST MOLECULAR & CELL BIOLOGY.
PA   (EHRL/) EHRLICH G.

Query Match             6.2%;
Best Local Similarity  23.8%;  Score 74.5;  DB 5;  Pred. No. 3.7e+02;  Length 3010;

RESULT 908
ID   ADF07294 standard; protein; 154 AA.
DE   Bacterial polypeptide #3407.
PN   US605709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.

Query Match             6.2%;
Best Local Similarity  26.4%;  Score 74.5;  DB 7;  Pred. No. 6.8;  Length 154;

RESULT 909
ID   ABU70365 standard; protein; 231 AA.
DE   Human adipocyte bait protein, melatonin receptor_V4.
PN   WO020286122-A2.
PD   31-OCT-2002.
PA   (HYBR-) HYBRIGENICS.

Query Match             6.2%;
Best Local Similarity  18.5%;  Score 74;  DB 6;  Pred. No. 12;  Length 231;

RESULT 910
ID   ABU70366 standard; protein; 231 AA.
DE   Human adipocyte bait protein, melatonin receptor_V5.
PN   WO020286122-A2.
PD   31-OCT-2002.
PA   (HYBR-) HYBRIGENICS.

Query Match             6.2%;
Best Local Similarity  18.5%;  Score 74;  DB 6;  Pred. No. 12;  Length 231;

RESULT 911
ID   ABB54180 standard; protein; 312 AA.
DE   Lactococcus lactis protein yiiG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.

Query Match             6.2%;
Best Local Similarity  24.3%;  Score 74;  DB 5;  Pred. No. 18;  Length 312;

RESULT 912
ID   ADS44483 standard; protein; 312 AA.
DE   Bacterial polypeptide #22913.
PN   US200323367S-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.

Query Match             6.2%;
Best Local Similarity  38.3%;  Score 74;  DB 8;  Pred. No. 18;  Length 312;

RESULT 913
ID   ABU02869 standard; protein; 324 AA.
DE   S. pneumoniae type 4 strain protein from coding region #2450.
PN   WO020277021-A2.
PD   03-OCT-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.

Query Match             6.2%;
Best Local Similarity  24.3%;  Score 74;  DB 6;  Pred. No. 19;  Length 324;

RESULT 914
ID   ADR94027 standard; protein; 332 AA.
DE   Novel S. pneumoniae protein sequence, SEQ ID 2662.
PN   US600744-B1.
PD   05-OCT-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.

Query Match             6.2%;
Best Local Similarity  24.3%;  Score 74;  DB 8;  Pred. No. 20;  Length 332;

RESULT 915
ID   AEA57897 standard; protein; 332 AA.
DE   Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:2662.
PN   US200516404-A1.
PD   23-JUN-2005.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.

Query Match             6.2%;
Best Local Similarity  24.3%;  Score 74;  DB 9;  Pred. No. 20;  Length 332;

RESULT 916
ID   AB000448 standard; protein; 342 AA.
DE   Novel human polypeptide #35.
PN   WO003023013-A2.
PD   20-MAR-2003.
PA   (HYSE-) HYSEQ INC.

Query Match             6.2%;
Best Local Similarity  21.2%;  Score 74;  DB 2;  Pred. No. 21;  Length 342;

RESULT 917
ID   AAR88412 standard; protein; 350 AA.
DE   High-affinity melatonin melatonin-1a receptor.
PN   WO9535320-A1.
PD   28-DEC-1995.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.

Query Match             6.2%;
Best Local Similarity  18.5%;  Score 74;  DB 2;  Pred. No. 21;  Length 350;

RESULT 918
ID   AAW15786 standard; protein; 350 AA.
DE   Melatonin receptor protein.
PN   JP09084581-A.
PD   31-MAR-1997.
PA   (TAKE ) TAKEDA CHEM IND LTD.

Query Match             6.2%;
Best Local Similarity  18.5%;  Score 74;  DB 2;  Pred. No. 21;  Length 350;

RESULT 919
ID   AAW94761 standard; protein; 350 AA.
DE   Human melatonin receptor type 1a protein mel-1a.
PN   EP892046-A2.
PD   20-JAN-1999.
PA   (JCRP-) JCR PHARM CO LTD.

Query Match             6.2%;
Best Local Similarity  18.5%;  Score 74;  DB 2;  Pred. No. 21;  Length 350;

RESULT 920
ID   ABP81840 standard; protein; 350 AA.
DE   Human melatonin receptor type 1a protein SEQ ID NO:164.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.

Query Match             6.2%;
Best Local Similarity  18.5%;  Score 74;  DB 6;  Pred. No. 21;  Length 350;

RESULT 921
ID   ADO29552 standard; protein; 350 AA.
DE   Human GPCR MTNR1A, SEQ ID NO:654.
PN   WO20040400000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.

Query Match             6.2%;
Best Local Similarity  18.5%;  Score 74;  DB 8;  Pred. No. 21;  Length 350;

RESULT 922
ID   AEC08362 standard; protein; 350 AA.
DE   Human melatonin receptor type 1A (MTNR1A).
PN   WO200507845S-A1.
PD   25-AUG-2005.
PA   (FARB) BAYER HEALTHCARE AG.

Query Match             6.2%;
Best Local Similarity  18.5%;  Score 74;  DB 9;  Pred. No. 21;  Length 350;

RESULT 923
ID   AAW19220 standard; protein; 364 AA.
DE   Rat growth hormone secretagogue receptor type Ia.
PN   WO9721730-A1.
PD   19-JUN-1997.

PA (MERI ) MERCK & CO INC.
Query Match 6.2%;
Best Local Similarity 19.4%; Score 74; DB 2; Pred. No. 22; Length 364;

RESULT 924
ID ABM73179 standard; protein; 366 AA.
DE Staphylococcus aureus protein #2419.
PN WO20094868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.2%;
Best Local Similarity 21.8%; Score 74; DB 6; Pred. No. 23; Length 366;

RESULT 925
ID ABB55224 standard; protein; 442 AA.
DE Lactococcus lactis protein yteD.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.2%;
Best Local Similarity 20.4%; Score 74; DB 5; Pred. No. 29; Length 442;

RESULT 926
ID ADN23927 standard; protein; 485 AA.
DE Bacterial polypeptide #6580.
PN US200323675-A1.
PD 18-DEC-2003.
PA (GOLD/) GOLDMAN B S.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
Query Match 6.2%;
Best Local Similarity 26.2%; Score 74; DB 8; Pred. No. 33; Length 485;

RESULT 927
ID AAY80509 standard; protein; 492 AA.
DE F. lutescens L-lysine:2-oxoglutarate 6-aminotransferase.
PN WO200008170-A1.
PD 17-FEB-2000.
PA (SAOC ) MERCIAN CORP.
Query Match 6.2%;
Best Local Similarity 22.5%; Score 74; DB 3; Pred. No. 34; Length 492;

RESULT 928
ID AAG64105 standard; protein; 493 AA.
DE Flavobacterium lutescens L-lysine-6-aminotransferase.
PN WO200148216-A1.
PD 05-JUL-2001.
PA (SAOC ) MERCIAN CORP.
Query Match 6.2%;
Best Local Similarity 22.5%; Score 74; DB 4; Pred. No. 34; Length 493;

RESULT 929
ID AAR54067 standard; protein; 1031 AA.
DE Non-A, non-B hepatitis virus gene #6 product.
PN JP06141870-A.
PD 24-MAY-1994.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA (SANW ) SANWA KAGAKU KENKYUSHO CO.
PA (TOFU ) TONEN CORP.
Query Match 6.2%;
Best Local Similarity 26.2%; Score 74; DB 2; Pred. No. 95; Length 1031;

RESULT 930
ID AAR98362 standard; protein; 1031 AA.
DE 5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#6).
PN JP07133291-A.
PD 23-MAY-1995.
PA (TOFU ) TONEN CORP.
Query Match 6.2%;
Best Local Similarity 26.2%; Score 74; DB 2; Pred. No. 95; Length 1031;

RESULT 931
ID AAG59839 standard; protein; 120 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77442.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%;
Best Local Similarity 20.3%; Score 73.5; DB 3; Pred. No. 5.5; Length 120;

RESULT 932
ID AAU25578 standard; protein; 192 AA.
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #25.
PN WO200162797-A2.
PD 30-AUG-2001.
PA (PHAA ) PHARMACIA & UPJOHN CO.
Query Match 6.2%;
Best Local Similarity 26.3%; Score 73.5; DB 4; Pred. No. 11; Length 192;

RESULT 933
ID ADU08915 standard; protein; 226 AA.
DE Coronavirus membrane protein seqid 38.
PN WO200496842-A2.
PD 11-NOV-2004.
PA (BCCA-) BC CANCER AGENCY.
Query Match 6.2%;
Best Local Similarity 22.2%; Score 73.5; DB 8; Pred. No. 13; Length 226;

RESULT 934
ID ABU44044 standard; protein; 268 AA.
DE Protein encoded by Prokaryotic essential gene #29571.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%;
Best Local Similarity 19.6%; Score 73.5; DB 6; Pred. No. 17; Length 268;

RESULT 935
ID AAG32488 standard; protein; 282 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39200.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%;
Best Local Similarity 28.1%; Score 73.5; DB 3; Pred. No. 18; Length 282;

RESULT 936
ID ADF05982 standard; protein; 312 AA.
DE Bacterial polypeptide #2095.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%;
Best Local Similarity 28.1%; Score 73.5; DB 7; Pred. No. 21; Length 312;

RESULT 937
ID AAG51386 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65212.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%;
Best Local Similarity 17.4%; Score 73.5; DB 3; Pred. No. 27; Length 377;

RESULT 938
ID AAG32487 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39199.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%;
Best Local Similarity 23.3%; Score 73.5; DB 9; Pred. No. 27; Length 377;

RESULT 939
ID ABM92289 standard; protein; 400 AA.
DE M. xanthus protein sequence, seq id 11488.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS ) MONSANTO TECHNOLOGY LLC.
Query Match 6.2%;
Best Local Similarity 28.1%; Score 73.5; DB 3; Pred. No. 29; Length 400;

RESULT 940
ID ADQ75734 standard; protein; 404 AA.
DE Codon optimised hCMV IE1 encoded exons 2 and 4.
PN WO2004058166-A2.
PD 15-JUL-2004.
PA (VICA-) VICAL INC.
Query Match 6.2%;
Best Local Similarity 23.3%; Score 73.5; DB 3; Pred. No. 30; Length 404;

RESULT 941
ID AAG51385 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65211.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%;
Best Local Similarity 19.3%; Score 73.5; DB 8; Pred. No. 30; Length 442;

RESULT 942
ID   AAG32486 standard; protein; 442 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39198.
PN   EP1033405-A2.
PD   06-SEP-2000.
Query Match              6.2%;   Score 73.5;   DB 3;   Pred. No. 34;
  Best Local Similarity  28.1%;   Score 73.5;   DB 3;   Length 442;

RESULT 943
ID   AAG51184 standard; protein; 489 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 65210.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (KERN/) KERN F.
Query Match              6.2%;   Score 73.5;   DB 3;   Pred. No. 34;
  Best Local Similarity  28.1%;   Score 73.5;   DB 3;   Length 489;

RESULT 944
ID   AAB86544 standard; protein; 491 AA.
DE   Human cytomegalovirus strain AD169 IE1 protein.
PN   WO200163286-A2.
PD   30-AUG-2001.
Query Match              6.2%;   Score 73.5;   DB 3;   Pred. No. 39;
  Best Local Similarity  28.1%;   Score 73.5;   DB 3;   Length 491;

RESULT 945
ID   ADP12517 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #127.
PN   WO200404346-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match              6.2%;   Score 73.5;   DB 4;   Pred. No. 39;
  Best Local Similarity  19.3%;   Score 73.5;   DB 4;   Length 491;

RESULT 946
ID   ADP12518 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #128.
PN   WO200404346-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match              6.2%;   Score 73.5;   DB 8;   Pred. No. 39;
  Best Local Similarity  19.3%;   Score 73.5;   DB 8;   Length 491;

RESULT 947
ID   ADP12513 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #123.
PN   WO200404346-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match              6.2%;   Score 73.5;   DB 8;   Pred. No. 39;
  Best Local Similarity  19.3%;   Score 73.5;   DB 8;   Length 491;

RESULT 948
ID   ADP12514 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #124.
PN   WO200404346-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match              6.2%;   Score 73.5;   DB 8;   Pred. No. 39;
  Best Local Similarity  19.3%;   Score 73.5;   DB 8;   Length 491;

RESULT 949
ID   ADQ75725 standard; protein; 491 AA.
DE   Wild type hCMV IE1.
PN   WO200458166-A2.
PD   15-JUL-2004.
PA   (VICA-) VICAL INC.
Query Match              6.2%;   Score 73.5;   DB 8;   Pred. No. 39;
  Best Local Similarity  19.3%;   Score 73.5;   DB 8;   Length 491;

RESULT 950
ID   ABP7574 standard; protein; 574 AA.
DE   Candida albicans essential protein SEQ ID NO 7411.
PN   WO200253728-A2.
PD   11-JUL-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match              6.2%;   Score 73.5;   DB 5;   Pred. No. 48;
  Best Local Similarity  19.3%;   Score 73.5;   DB 5;   Length 574;

RESULT 951
Query Match              6.2%;   Score 73.5;   DB 5;   Pred. No. 48;
  Best Local Similarity  20.8%;   Score 73.5;   DB 5;   Length 574;

RESULT 952
ID   AED26251 standard; protein; 577 AA.
DE   Novel human full-length polypeptide 791CIP2B_12, SEQ ID NO:247.
PN   US2005221342-A1.
PD   06-OCT-2005.
PA   (NUVE-) NUVELO INC.
Query Match              6.2%;   Score 73.5;   DB 2;   Pred. No. 49;
  Best Local Similarity  20.8%;   Score 73.5;   DB 9;   Length 577;

RESULT 953
ID   ADS28278 standard; protein; 637 AA.
DE   Bacterial polypeptide #17311.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (NUVE-) NUVELO INC.
PA   (CAO/)  CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match              6.2%;   Score 73.5;   DB 2;   Pred. No. 56;
  Best Local Similarity  20.8%;   Score 73.5;   DB 9;   Length 637;

RESULT 954
ID   ABG29128 standard; protein; 682 AA.
DE   Novel human diagnostic protein #29119.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Query Match              6.2%;   Score 73.5;   DB 4;   Pred. No. 62;
  Best Local Similarity  20.0%;   Score 73.5;   DB 4;   Length 682;

RESULT 955
ID   ABB61737 standard; protein; 1287 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 12003.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Query Match              6.2%;   Score 73.5;   DB 1;   Pred. No. 1.5e+02;
  Best Local Similarity  18.2%;   Score 73.5;   DB 4;   Length 1287;

RESULT 956
ID   ADS96670 standard; protein; 1287 AA.
DE   Drosophila melanogaster protein, SEQ ID NO 291.
PN   WO200439999-A2.
PD   13-MAY-2004.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match              6.2%;   Score 73.5;   DB 1;   Pred. No. 1.5e+02;
  Best Local Similarity  18.2%;   Score 73.5;   DB 8;   Length 1287;

RESULT 957
ID   AAR33214 standard; protein; 3033 AA.
DE   NANBH virus strain HC-J8 protein.
PN   EP532167-A2.
PD   17-MAR-1993.
PA   (IMMO ) IMMUNO JAPAN INC.
Query Match              6.2%;   Score 73.5;   DB 1;   Pred. No. 4.9e+02;
  Best Local Similarity  18.2%;   Score 73.5;   DB 8;   Length 3033;

RESULT 958
ID   ABY03151 standard; protein; 7176 AA.
DE   Murine hepatitis virus strain pol lab protein, SEQ:9897.
PN   WO200409360-A2.
PD   28-OCT-2004.
PA   (CHIR ) CHIRON CORP.
Query Match              6.2%;   Score 73.5;   DB 1;   Pred. No. 1.6e+03;
  Best Local Similarity  26.4%;   Score 73.5;   DB 2;   Length 7176;

RESULT 959
ID   AAW20571 standard; protein; 114 AA.
DE   H. Pylori secreted or periplasmic protein 80257.aa.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (ASTR ) ASTRA AB.
Query Match              6.1%;   Score 73;   DB 2;   Pred. No. 5.9;
  Best Local Similarity  27.4%;   Score 73.5;   DB 2;   Length 114;

ID   AAU69567 standard; protein; 189 AA.
DE   Human G protein-coupled receptor from cDNA Seq-2643.
PN   WO200177330-A2.
PD   18-OCT-2001.
PA   (PHA ) PHARMACIA & UPJOHN CO.
Query Match              6.2%;   Score 73;   DB 2;   Pred. No. 21.6;
  Best Local Similarity  21.6%;   Score 73;   DB 2;   Length 189;

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Query Match
Best Local Similarity  20.3%; Score 73; Pred. No. 12; DB 5; Length 189;
ID   ADC97146 standard; protein; 199 AA.
DE   E. faecium protein sequence SEQ ID 6773.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
RESULT 960
Query Match
Best Local Similarity  22.6%; Score 73; Pred. No. 13; DB 7; Length 199;
ID   ABP29367 standard; protein; 249 AA.
DE   Streptococcus polypeptide SEQ ID NO 7910.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
RESULT 961
Query Match
Best Local Similarity  24.6%; Score 73; Pred. No. 17; DB 5; Length 249;
ID   AAU87836 standard; protein; 272 AA.
DE   T. aureum 7091 elongase TEL01 from plasmid pRAT-4-A1.
PN   WO200208401-A2.
PD   31-JAN-2002.
PA   (ABBO ) ABBOTT LAB.
RESULT 962
Query Match
Best Local Similarity  19.9%; Score 73; Pred. No. 20; DB 5; Length 272;
ID   ADH80191 standard; protein; 272 AA.
DE   Fungal 7091 elongase protein seq id 75.
PN   US20030163845-A1.
PD   28-AUG-2003.
PA   (MUKE/) MUKERJI P.
PA   (LEON/) EUN-YEONG LEONARD A.
RESULT 963
Query Match
Best Local Similarity  19.9%; Score 73; Pred. No. 20; DB 8; Length 272;
ID   ADW12982 standard; protein; 272 AA.
DE   Elongase protein #55.
PN   US20050009140-A1.
PD   13-JAN-2005.
PA   (MUKE/) MUKERJI P.
PA   (LEON/) LEONARD A E.
PA   (HUAN/) HUANG Y.
PA   (PERE/) PEREIRA S L.
RESULT 964
Query Match
Best Local Similarity  19.9%; Score 73; Pred. No. 20; DB 9; Length 272;
ID   ABM73154 standard; protein; 290 AA.
DE   Staphylococcus aureus protein #2394.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
RESULT 965
Query Match
Best Local Similarity  23.4%; Score 73; Pred. No. 22; DB 6; Length 290;
ID   ABR47464 standard; protein; 322 AA.
DE   Breast cancer associated protein sequence SEQ ID NO:160.
PN   WO200300989-A2.
PD   16-JAN-2003.
PA   (MILL-) MILLENIUM PHARM INC.
RESULT 966
Query Match
Best Local Similarity  20.6%; Score 73; Pred. No. 25; DB 6; Length 322;
ID   ADN61865 standard; protein; 349 AA.
DE   Human novel protein NOV42a.
PN   US20040043382-A1.
PD   04-MAR-2004.
PA   (PADI/) PADIGARU M.
PA   (SPYT/) SPYTEK K A.
PA   (SHEN/) SHENOY S G.
PA   (TAUP/) TAUPIER R J.
PA   (PENA/) PENA C E A.
PA   (LILL/) LI L.
PA   (ZERH/) ZERHUSEN B D.
PA   (GUSE/) GUSEV V Y.
PA   (JIWW/) JI W.
PA   (GORM/) GORMAN L.
PA   (MILL/) MILLER C E.
PA   (KEKU/) KEKUDA R.
PA   (PATT/) PATTURAJAN M.
PA   (GANG/) GANGOLLI E A.
PA   (GANG/) GANGOLLI E A.
PA   (VERN/) VERNET C A M.
PA   (GUOX/) GUO X S.
PA   (TCHE/) TCHERNEV V T.
PA   (FERN/) FERNANDES E R.
PA   (CASM/) CASMAN S J.
PA   (MALY/) MALYANKAR U M.
PA   (GERL/) GERLACH V.
PA   (LIUY/) LIU Y.
PA   (ANDE/) ANDERSON D W.
PA   (SPAD/) SPADERNA S K.
PA   (CATT/) CATTERTON E.
PA   (LEIT/) LEITE M W.
PA   (ZHON/) ZHONG H.
PA   (ALSO/) ALSOBROOK J P.
PA   (LEPL/) LEPLEY D M.
PA   (RIEG/) RIEGER D K.
PA   (BURG/) BURGESS C E.
RESULT 967
Query Match
Best Local Similarity  24.0%; Score 73; Pred. No. 28; DB 8; Length 349;
ID   AAW19613 standard; protein; 364 AA.
DE   Rat growth hormone secretagogue receptor type Ia.
PN   WO9722004-A1.
PD   19-JUN-1997.
PA   (MERI ) MERCK & CO INC.
RESULT 968
Query Match
Best Local Similarity  19.4%; Score 73; Pred. No. 29; DB 2; Length 364;
ID   AAY54565 standard; protein; 364 AA.
DE   A mouse growth hormone secretagogue receptor.
PN   WO200002918-A1.
PD   20-JAN-2000.
PA   (MERI ) MERCK & CO INC.
RESULT 969
Query Match
Best Local Similarity  19.4%; Score 73; Pred. No. 29; DB 3; Length 364;
ID   AAB97377 standard; protein; 364 AA.
DE   Rat growth hormone secretagogue receptor (GHSR) related protein.
PN   WO200112705-A1.
PD   10-MAY-2001.
PA   (TAKE ) TAKEDA CHEM IND LTD.
RESULT 970
Query Match
Best Local Similarity  19.4%; Score 73; Pred. No. 29; DB 4; Length 364;
ID   ADO29026 standard; protein; 364 AA.
DE   Mouse novel GPCR GHSR, SEQ ID NO:125.
PN   WO200400000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
RESULT 971
Query Match
Best Local Similarity  19.4%; Score 73; Pred. No. 29; DB 8; Length 364;
ID   AAW77773 standard; protein; 377 AA.
DE   Staphylococcus aureus protein of unknown function.
PN   EP841394-A2.
PD   13-MAY-1998.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
RESULT 972
Query Match
Best Local Similarity  23.3%; Score 73; Pred. No. 31; DB 2; Length 377;
ID   AAG50065 standard; protein; 415 AA.
RESULT 973
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(continuation of preceding result)
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 63404.
PN  EP1033405-A2.
PD  06-SEP-2000.
    Query Match             6.1%;  Score 73;  DB 3;  Length 415;
    Best Local Similarity  19.8%;  Pred. No. 35;

RESULT 974
ID  AAG24013 standard; protein; 427 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 27528.
PN  EP1033405-A2.
PD  06-SEP-2000.
    Query Match             6.1%;  Score 73;  DB 3;  Length 427;
    Best Local Similarity  22.0%;  Pred. No. 37;

RESULT 975
ID  AAG24012 standard; protein; 430 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 27527.
PN  EP1033405-A2.
PD  06-SEP-2000.
    Query Match             6.1%;  Score 73;  DB 3;  Length 430;
    Best Local Similarity  22.0%;  Pred. No. 37;

RESULT 976
ID  ABU31419 standard; protein; 453 AA.
DE  Protein encoded by Prokaryotic essential gene #16946.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
    Query Match             6.1%;  Score 73;  DB 6;  Length 453;
    Best Local Similarity  26.5%;  Pred. No. 40;

RESULT 977
ID  AEA16981 standard; protein; 469 AA.
DE  Arabidopsis thaliana protein #40.
PN  US200512515159-A1.
PD  09-JUN-2005.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (STEI/) STEIN J C.
PA  (CAOY/) CAO Y.
    Query Match             6.1%;  Score 73;  DB 9;  Length 469;
    Best Local Similarity  26.5%;  Pred. No. 42;

RESULT 978
ID  AAG50064 standard; protein; 472 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 63403.
PN  EP1033405-A2.
PD  06-SEP-2000.
    Query Match             6.1%;  Score 73;  DB 3;  Length 472;
    Best Local Similarity  19.8%;  Pred. No. 42;

RESULT 979
ID  AAG50063 standard; protein; 474 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 63402.
PN  EP1033405-A2.
PD  06-SEP-2000.
    Query Match             6.1%;  Score 73;  DB 3;  Length 474;
    Best Local Similarity  19.8%;  Pred. No. 43;

RESULT 980
ID  ABM70313 standard; protein; 490 AA.
DE  Photorhabdus luminescens protein sequence #3410.
PN  WO200294867-A2.
PD  28-NOV-2002.
PA  (CNRS ) CNRS CENT NAT RECH SCI.
PA  (INSP ) INST PASTEUR.
    Query Match             6.1%;  Score 73;  DB 6;  Length 490;
    Best Local Similarity  19.8%;  Pred. No. 45;

RESULT 981
ID  AAY33766 standard; protein; 495 AA.
DE  hKv5.1 human brain-specific potassium channel.
PN  WO9941372-A1.
PD  19-AUG-1999.
PA  (ZENE ) ZENECA LTD.
    Query Match             6.1%;  Score 73;  DB 6;  Length 495;
    Best Local Similarity  24.6%;  Pred. No. 45;

RESULT 982
ID  AB063300 standard; protein; 501 AA.
DE  Klebsiella pneumoniae polypeptide seqid 9817.
PN  US6610836-B1.
PD  26-AUG-2003.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match             6.1%;  Score 73;  DB 2;  Length 501;
    Best Local Similarity  23.2%;  Pred. No. 45;

(continuation)
    Query Match             6.1%;  Score 73;  DB 7;  Length 501;
    Best Local Similarity  26.5%;  Pred. No. 46;

RESULT 983
ID  ABP53583 standard; protein; 526 AA.
DE  Human NOV13b protein SEQ ID NO:30.
PN  WO200262999-A2.
PD  15-AUG-2002.
PA  (CURA-) CURAGEN CORP.
    Query Match             6.1%;  Score 73;  DB 5;  Length 526;
    Best Local Similarity  23.3%;  Pred. No. 49;

RESULT 984
ID  ADH42229 standard; protein; 526 AA.
DE  Novel human protein NOV50d.
PN  WO200310215159-A2.
PD  11-DEC-2003.
PA  (CURA-) CURAGEN CORP.
    Query Match             6.1%;  Score 73;  DB 8;  Length 526;
    Best Local Similarity  23.3%;  Pred. No. 49;

RESULT 985
ID  ABU31136 standard; protein; 553 AA.
DE  Protein encoded by Prokaryotic essential gene #16663.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
    Query Match             6.1%;  Score 73;  DB 6;  Length 553;
    Best Local Similarity  19.6%;  Pred. No. 53;

RESULT 986
ID  AAG24011 standard; protein; 556 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 27526.
PN  EP1033405-A2.
PD  06-SEP-2000.
    Query Match             6.1%;  Score 73;  DB 3;  Length 556;
    Best Local Similarity  22.0%;  Pred. No. 53;

RESULT 987
ID  ADQ96000 standard; protein; 608 AA.
DE  T cell activation associated protein #89.
PN  WO200405880S-A2.
PD  15-JUL-2004.
PA  (ASAH-) ASAHI KASEI PHARMA CORP.
    Query Match             6.1%;  Score 73;  DB 8;  Length 608;
    Best Local Similarity  19.5%;  Pred. No. 60;

RESULT 988
ID  ADR99134 standard; protein; 635 AA.
DE  Human protein similar to yeast SSM4, TEB4, SEQ ID 140.
PN  WO200407803S-A2.
PD  16-SEP-2004.
PA  (FARB ) BAYER PHARM CORP.
    Query Match             6.1%;  Score 73;  DB 8;  Length 635;
    Best Local Similarity  19.5%;  Pred. No. 64;

RESULT 989
ID  ABB71311 standard; protein; 717 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 40725.
PN  WO200171042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
    Query Match             6.1%;  Score 73;  DB 4;  Length 717;
    Best Local Similarity  21.3%;  Pred. No. 76;

RESULT 990
ID  AAW26673 standard; protein; 746 AA.
DE  Staphylococcus aureus spoIIIE protein.
PN  WO9726338-A1.
PD  24-JUL-1997.
PA  (SMIK ) SMITHKLINE BEECHAM PLC.
    Query Match             6.1%;  Score 73;  DB 2;  Length 746;
    Best Local Similarity  23.3%;  Pred. No. 80;

RESULT 991
ID  AAU37199 standard; protein; 748 AA.
DE  Staphylococcus aureus cellular proliferation protein #1369.
PN  WO200170955-A2.
PD  27-SEP-2001.
PA  (ELIT-) ELITRA PHARM INC.
    Query Match             6.1%;  Score 73;  DB 4;  Length 748;
    Best Local Similarity  23.3%;  Pred. No. 80;

RESULT 992
ID   AAW88407 standard; protein; 750 AA.
DE   Human adult neural tissue secreted protein s195_10.
PN   WO9857976-A1.
PD   23-DEC-1998.
PA   (GEMY) GENETICS INST INC.
     Query Match             19.5%;  Score 73;  DB 2;  Length 750;
     Best Local Similarity

RESULT 993
ID   AED72894 standard; protein; 750 AA.
DE   Human clone s195_10 encoding cDNA SEQ ID NO:86.
PN   US2005250180-A1.
PD   10-NOV-2005.
PA   (JACO/) JACOBS K.
PA   (MCCO/) MCCOY J M.
PA   (LAVA/) LAVALLIE E R.
PA   (COLL/) COLLINS-RACIE L A.
PA   (EVAN/) EVANS C.
PA   (MERB/) MERBERG D.
PA   (TREA/) TREACY M.
PA   (SPAU/) SPAULDING V.
     Query Match             19.5%;  Score 73;  DB 9;  Length 750;
     Best Local Similarity

RESULT 994
ID   AAW26672 standard; protein; 788 AA.
DE   Staphylococcus aureus spoIIE protein.
PN   WO9726338-A1.
PD   24-JUL-1997.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
     Query Match             23.3%;  Score 73;  DB 2;  Length 788;
     Best Local Similarity

RESULT 995
ID   ABU42392 standard; protein; 788 AA.
DE   Protein encoded by Prokaryotic essential gene #27919.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             23.3%;  Score 73;  DB 6;  Length 788;
     Best Local Similarity

RESULT 996
ID   AAU36734 standard; protein; 792 AA.
DE   Staphylococcus aureus cellular proliferation protein #904.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             23.3%;  Score 73;  DB 4;  Length 792;
     Best Local Similarity

RESULT 997
ID   ABJ19057 standard; protein; 792 AA.
DE   Pathogen specific antigen related staphylococcal protein SEQ ID NO 334.
PN   WO2002259148-A2.
PD   01-AUG-2002.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
     Query Match             23.3%;  Score 73;  DB 6;  Length 792;
     Best Local Similarity

RESULT 998
ID   ABM73117 standard; protein; 792 AA.
DE   Staphylococcus aureus protein #2357.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match             23.3%;  Score 73;  DB 6;  Length 792;
     Best Local Similarity

RESULT 999
ID   AAW60466 standard; protein; 845 AA.
DE   Protein encoded by fragment #6 isolated from Hepatitis C virus genome.
PN   WO9825960-A1.
PD   18-JUN-1998.
PA   (INGE-) CENT ING GENETICA & BIOTECNOLOGIA.
     Query Match             26.2%;  Score 73;  DB 2;  Length 845;
     Best Local Similarity

RESULT 1000
ID   ADQ95946 standard; protein; 910 AA.

DE   T cell activation associated protein #62.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match             19.5%;  Score 73;  DB 8;  Length 910;
     Best Local Similarity

RESULT 1001
ID   ABG24246 standard; protein; 913 AA.
DE   Novel human diagnostic protein #24237.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             19.5%;  Score 73;  DB 4;  Length 913;
     Best Local Similarity

RESULT 1002
ID   AAM51861 standard; protein; 966 AA.
DE   Murine polycystic kidney disease protein 2.
PN   WO200177331-A1.
PD   18-OCT-2001.
PA   (MILL-) MILLENIUM PHARM INC.
     Query Match             21.3%;  Score 73;  DB 5;  Length 966;
     Best Local Similarity

RESULT 1003
ID   ABB07819 standard; protein; 966 AA.
DE   Mouse polycystic kidney disease protein 2.
PN   US2002035056-A1.
PD   21-MAR-2002.
PA   (CURT/) CURTIS R A J.
PA   (SILO/) SILOS-SANTIAGO I.
     Query Match             21.3%;  Score 73;  DB 5;  Length 966;
     Best Local Similarity

RESULT 1004
ID   ADJ76159 standard; protein; 966 AA.
DE   Marker gene related amino acid sequence SEQ ID NO:1411.
PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (GENO-) GENOX RES INC.
     Query Match             21.3%;  Score 73;  DB 8;  Length 966;
     Best Local Similarity

RESULT 1005
ID   ADV66235 standard; protein; 966 AA.
DE   Polycystic kidney disease protein 2, SEQ ID 11.
PN   US2004248160-A1.
PD   09-DEC-2004.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match             21.3%;  Score 73;  DB 9;  Length 966;
     Best Local Similarity

RESULT 1006
ID   ADZ26335 standard; protein; 966 AA.
DE   Human hypoxia-responsive protein CNGH0002.1.
PN   WO2005033293-A2.
PD   14-APR-2005.
PA   (CENZ ) CENTOCOR INC.
     Query Match             21.3%;  Score 73;  DB 9;  Length 966;
     Best Local Similarity

RESULT 1007
ID   ABG05866 standard; protein; 971 AA.
DE   Novel human diagnostic protein #5857.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             19.5%;  Score 73;  DB 4;  Length 971;
     Best Local Similarity

RESULT 1008
ID   ADR99135 standard; protein; 971 AA.
DE   Human protein similar to yeast SSM4, TEB4, SEQ ID 141.
PN   WO2004078035-A2.
PD   16-SEP-2004.
PA   (FARB ) BAYER PHARM CORP.
     Query Match             19.5%;  Score 73;  DB 8;  Length 971;
     Best Local Similarity

RESULT 1009
ID   ADZ11480 standard; protein; 971 AA.

DE   MARCH VI protein, SEQ ID 49.
PN   US200507961J-A1.
PD   14-APR-2005.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
     Query Match             6.1%;  Score 73;  DB 9;  Length 971;
     Best Local Similarity   19.5%;  Pred. No. 1.1e+02;
RESULT 1010
ID   ADZ11490 standard; protein; 971 AA.
DE   MARCH VI protein, SEQ ID 59.
PN   US200507961J-A1.
PD   14-APR-2005.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
     Query Match             6.1%;  Score 73;  DB 9;  Length 971;
     Best Local Similarity   19.5%;  Pred. No. 1.1e+02;
RESULT 1011
ID   ABG07373 standard; protein; 976 AA.
DE   Novel human diagnostic protein #7364.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             6.1%;  Score 73;  DB 9;  Length 976;
     Best Local Similarity   19.5%;  Pred. No. 1.2e+02;
RESULT 1012
ID   ADX40795 standard; protein; 3010 AA.
DE   HCV polymerase protein #18.
PN   WO200512502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.
     Query Match             6.1%;  Score 73;  DB 9;  Length 3010;
     Best Local Similarity   26.2%;  Pred. No. 5.5e+02;
RESULT 1013
ID   ABU05456 standard; protein; 209 AA.
DE   M. tuberculosis and M. leprae marker protein #107.
PN   WO200274903-A2.
PD   26-SEP-2002.
PA   (INSP ) INST PASTEUR.
     Query Match             6.1%;  Score 72.5;  DB 5;  Length 209;
     Best Local Similarity   22.1%;  Pred. No. 16;
RESULT 1014
ID   ABU15302 standard; protein; 222 AA.
DE   Protein encoded by Prokaryotic essential gene #829.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.1%;  Score 72.5;  DB 6;  Length 222;
     Best Local Similarity   20.5%;  Pred. No. 17;
RESULT 1015
ID   ADY24595 standard; protein; 274 AA.
DE   Plant full length insert polypeptide seqid 72379.
PN   US200403488-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 274;
     Best Local Similarity   26.5%;  Pred. No. 23;
RESULT 1016
ID   ADX95386 standard; protein; 274 AA.
DE   Plant full length insert polypeptide seqid 58050.
PN   US200403488-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 274;
     Best Local Similarity   26.5%;  Pred. No. 23;
RESULT 1017

ID   ABB53879 standard; protein; 307 AA.
DE   Lactococcus lactis protein yfgG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
     Query Match             6.1%;  Score 72.5;  DB 5;  Length 307;
     Best Local Similarity   22.9%;  Pred. No. 27;
RESULT 1018
ID   ADY10668 standard; protein; 307 AA.
DE   Plant full length insert polypeptide seqid 66483.
PN   US200403488-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 307;
     Best Local Similarity   25.3%;  Pred. No. 27;
RESULT 1019
ID   ADY11265 standard; protein; 307 AA.
DE   Plant full length insert polypeptide seqid 67080.
PN   US200403488-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 307;
     Best Local Similarity   25.3%;  Pred. No. 27;
RESULT 1020
ID   ADY10993 standard; protein; 307 AA.
DE   Plant full length insert polypeptide seqid 66808.
PN   US200403488-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 307;
     Best Local Similarity   25.3%;  Pred. No. 27;
RESULT 1021
ID   ADY11014 standard; protein; 308 AA.
DE   Plant full length insert polypeptide seqid 66829.
PN   US200403488-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 308;
     Best Local Similarity   25.3%;  Pred. No. 27;
RESULT 1022
ID   ADY10930 standard; protein; 310 AA.
DE   Plant full length insert polypeptide seqid 66745.
PN   US200403488-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 310;
     Best Local Similarity   25.3%;  Pred. No. 27;
RESULT 1023

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ID   ADY11546 standard; protein; 310 AA.
DE   Plant full length insert polypeptide seqid 67361.
PN   US20040384888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match
     Best Local Similarity   25.3%;   Score 72.5;   DB 8;   Length 310;

RESULT 1024
ID   ADY09462 standard; protein; 311 AA.
DE   Plant full length insert polypeptide seqid 65277.
PN   US20040384888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match
     Best Local Similarity   25.3%;   Score 72.5;   DB 8;   Length 311;

RESULT 1025
ID   ADY11115 standard; protein; 312 AA.
DE   Plant full length insert polypeptide seqid 66930.
PN   US20040384888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match
     Best Local Similarity   25.3%;   Score 72.5;   DB 8;   Length 312;

RESULT 1026
ID   ADY10946 standard; protein; 312 AA.
DE   Plant full length insert polypeptide seqid 66761.
PN   US20040384888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match
     Best Local Similarity   25.3%;   Score 72.5;   DB 8;   Length 312;

RESULT 1027
ID   ABB53675 standard; protein; 325 AA.
DE   Lactococcus lactis protein ydhB.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
     Query Match
     Best Local Similarity   25.9%;   Score 72.5;   DB 5;   Length 325;

RESULT 1028
ID   ADH87677 standard; protein; 353 AA.
DE   Enterococcus faecalis polypeptide #2157.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match
     Best Local Similarity   21.5%;   Score 72.5;   DB 7;   Length 353;

RESULT 1029
ID   ADH87557 standard; protein; 359 AA.
DE   Enterococcus faecalis polypeptide #2037.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match
     Best Local Similarity   25.0%;   Score 72.5;   DB 7;   Length 359;

RESULT 1030
ID   AAR37264 standard; protein; 389 AA.
DE   Oxytocin receptor.
PN   EP542424-A1.
PD   19-MAY-1993.
PA   (ROHT ) ROHTO PHARM CO LTD.
     Query Match
     Best Local Similarity   24.5%;   Score 72.5;   DB 2;   Length 389;

RESULT 1031
ID   AAW23832 standard; protein; 389 AA.
DE   Human oxytocin receptor.
PN   EP811684-A2.
PD   10-DEC-1997.
PA   (ROHT ) ROHTO PHARM CO LTD.
     Query Match
     Best Local Similarity   24.5%;   Score 72.5;   DB 2;   Length 389;

RESULT 1032
ID   AAM40217 standard; protein; 389 AA.
DE   Human polypeptide SEQ ID NO 3362.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match
     Best Local Similarity   24.5%;   Score 72.5;   DB 4;   Length 389;

RESULT 1033
ID   ABP81865 standard; protein; 389 AA.
DE   Human oxytocin receptor protein SEQ ID NO:215.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match
     Best Local Similarity   24.5%;   Score 72.5;   DB 6;   Length 389;

RESULT 1034
ID   AAE38317 standard; protein; 389 AA.
DE   Human oxytocin receptor protein.
PN   WO2003064402-A1.
PD   07-AUG-2003.
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
     Query Match
     Best Local Similarity   24.5%;   Score 72.5;   DB 6;   Length 389;

RESULT 1035
ID   ADP12125 standard; protein; 389 AA.
DE   Human oxytocin receptor (OXTR) protein SEQ ID NO:2.
PN   WO2003093816-A2.
PD   13-NOV-2003.
PA   (FARB ) BAYER AG.
     Query Match
     Best Local Similarity   24.5%;   Score 72.5;   DB 8;   Length 389;

RESULT 1036
ID   ADI03915 standard; protein; 389 AA.
DE   Human oxytocin receptor polypeptide.
PN   WO200400993-A2.
PD   31-DEC-2003.
PA   (UYQU-) UNIV QUEBEC A MONTREAL.
PA   (UYMO-) UNIV MONTREAL CENT HOSPITALIER.
     Query Match
     Best Local Similarity   24.5%;   Score 72.5;   DB 8;   Length 389;

RESULT 1037
ID   ADO29590 standard; protein; 389 AA.
DE   Human GPCR OXTR, SEQ ID NO:692.
PN   WO200040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match
     Best Local Similarity   24.5%;   Score 72.5;   DB 8;   Length 389;

RESULT 1038
ID   ADW98687 standard; protein; 389 AA.
DE   Human oxytocin receptor (OXTR) protein SeqID1.
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PN   WO2005012565-A1
PD   10-FEB-2005.
PA   (ASTR ) ASTRAZENECA AB.
PA   (ASTR ) ASTRAZENECA UK LTD.
Query Match
     Best Local Similarity  24.5%;  Score  72.5;  DB  9;  Pred. No.  37;  Length 389;

RESULT 1039
ID   AAR58665 standard; protein; 448 AA.
DE   Bovine PACAP receptor type 1B mature protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.
Query Match
     Best Local Similarity  29.6%;  Score  72.5;  DB  2;  Pred. No.  45;  Length 448;

RESULT 1040
ID   AAR58663 standard; protein; 476 AA.
DE   Bovine PACAP receptor type 1A mature protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.
Query Match
     Best Local Similarity  29.6%;  Score  72.5;  DB  2;  Pred. No.  49;  Length 476;

RESULT 1041
ID   AAR58657 standard; protein; 485 AA.
DE   Bovine PACAP receptor type 1B protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.
Query Match
     Best Local Similarity  29.6%;  Score  72.5;  DB  2;  Pred. No.  50;  Length 485;

RESULT 1042
ID   AAR58655 standard; protein; 513 AA.
DE   Bovine PACAP receptor type 1A protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.
Query Match
     Best Local Similarity  29.6%;  Score  72.5;  DB  2;  Pred. No.  54;  Length 513;

RESULT 1043
ID   ADN19765 standard; protein; 522 AA.
DE   Bacterial polypeptide #2418.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match
     Best Local Similarity  22.5%;  Score  72.5;  DB  8;  Pred. No.  56;  Length 522;

RESULT 1044
ID   ADV89115 standard; protein; 666 AA.
DE   Streptococcus agalactiae protein sequence, SEQ ID 1509.
PN   FR2824074-A1.
PD   31-OCT-2002.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
Query Match
     Best Local Similarity  23.1%;  Score  72.5;  DB  8;  Pred. No.  78;  Length 666;

RESULT 1045
ID   ADV82479 standard; protein; 666 AA.
DE   Streptococcus agalactiae protein, SEQ ID 3620.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
Query Match
     Best Local Similarity  23.1%;  Score  72.5;  DB  8;  Pred. No.  78;  Length 666;

RESULT 1046
ID   ADV80368 standard; protein; 666 AA.
DE   Streptococcus agalactiae protein, SEQ ID 1509.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
Query Match
     Best Local Similarity  23.1%;  Score  72.5;  DB  8;  Pred. No.  78;  Length 666;

RESULT 1047
ID   AD181620 standard; protein; 769 AA.
DE   C. elegans protein similar to Pfam PF00023.
PN   US2004009537-A1.
PD   15-JAN-2004.
PA   (ROOS/) ROOS J.
PA   (STAU/) STAUDERMAN K.
PA   (VELI/) VELICELEBI G.
PA   (REGC ) UNIV CALIFORNIA.
Query Match
     Best Local Similarity  20.2%;  Score  72.5;  DB  5;  Pred. No.  95;  Length 769;

RESULT 1048
ID   ABB05429 standard; protein; 848 AA.
DE   Arabidopsis thaliana ABH1 protein SEQ ID NO:2.
PN   WO200196585-A2.
PD   20-DEC-2001.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match
     Best Local Similarity  22.3%;  Score  72.5;  DB  6;  Pred. No.  1.1e+02;  Length 848;

RESULT 1049
ID   AAB31528 standard; protein; 848 AA.
DE   Arabidopsis thaliana protein used to isolate rice CBP80 orthologues.
PN   WO200281696-A2.
PD   17-OCT-2002.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match
     Best Local Similarity  22.3%;  Score  72.5;  DB  6;  Pred. No.  1.1e+02;  Length 848;

RESULT 1050
ID   ABU25159 standard; protein; 851 AA.
DE   Protein encoded by Prokaryotic essential gene #10686.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match
     Best Local Similarity  20.5%;  Score  72.5;  DB  6;  Pred. No.  1.1e+02;  Length 851;

RESULT 1051
ID   ADY10144 standard; protein; 903 AA.
DE   Plant full length insert polypeptide seqid 65959.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
Query Match
     Best Local Similarity  18.1%;  Score  72.5;  DB  8;  Pred. No.  1.2e+02;  Length 903;

RESULT 1052
ID   ADW76078 standard; protein; 1051 AA.
DE   Human cytomegalovirus (HCMV) pp65-IE1 fusion protein.
PN   WO200507689-A1.
PD   27-JAN-2005.
PA   (ALPH-) ALPHAVAX INC.
Query Match
     Best Local Similarity  19.3%;  Score  72.5;  DB  9;  Pred. No.  1.5e+02;  Length 1051;

RESULT 1053
ID   AAR34580 standard; protein; 3010 AA.
DE   Human hepatitis C virus gene encoded polypeptide.
PN   EP541089-A2.
PD   12-MAY-1993.
PA   (SANW ) SANWA KAGAKU KENKYUSHO CO.
Query Match
     Best Local Similarity  23.7%;  Score  72.5;  DB  2;  Pred. No.  6.3e+02;  Length 3010;

RESULT 1054
ID   ADQ96378 standard; protein; 208 AA.
DE   T cell activation associated protein #278.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.

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Query Match           6.0%;    Score 72; DB 8; Length 208;
Best Local Similarity 20.8%;   Pred. No. 18;
RESULT 1055
ID  AED36113 standard; protein; 260 AA.
DE  Tobacco NAP1-like protein (NtNAP1b).
PN  WO2005094562-A1.
PD  13-OCT-2005.
PA  (CROP-) CROPDESIGN NV.
Query Match           6.0%;    Score 72; DB 9; Length 260;
Best Local Similarity 31.6%;   Pred. No. 24;
RESULT 1056
ID  ABB48543 standard; protein; 306 AA.
DE  Listeria monocytogenes protein #1247.
PN  WO200177335-A2.
PD  18-OCT-2001.
PA  (INSP ) INST PASTEUR.
Query Match           6.0%;    Score 72; DB 5; Length 306;
Best Local Similarity 21.0%;   Pred. No. 30;
RESULT 1057
ID  ABU39432 standard; protein; 317 AA.
DE  Protein encoded by Prokaryotic essential gene #24959.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
Query Match           6.0%;    Score 72; DB 6; Length 317;
Best Local Similarity 23.5%;   Pred. No. 32;
RESULT 1058
ID  AAB53392 standard; protein; 334 AA.
DE  Human colon cancer antigen protein sequence SEQ ID NO:932.
PN  WO200055351-A1.
PD  21-SEP-2000.
PA  (HUMA-) HUMAN GENOME SCI INC.
Query Match           6.0%;    Score 72; DB 3; Length 334;
Best Local Similarity 28.8%;   Pred. No. 34;
RESULT 1059
ID  AAY87505 standard; protein; 370 AA.
DE  Human G coupled-protein receptor, hGR3.
PN  WO200017641-A1.
PD  30-MAR-2000.
PA  (MILL-) MILLENNIUM PHARM INC.
Query Match           6.0%;    Score 72; DB 3; Length 370;
Best Local Similarity 21.8%;   Pred. No. 40;
RESULT 1060
ID  AAW20731 standard; protein; 375 AA.
DE  H. Pylori inner membrane protein, 06cp1111l80rf6.
PN  WO9640893-A1.
PD  19-DEC-1996.
PA  (ASTR ) ASTRA AB.
Query Match           6.0%;    Score 72; DB 2; Length 375;
Best Local Similarity 20.9%;   Pred. No. 40;
RESULT 1061
ID  ABU19932 standard; protein; 396 AA.
DE  Protein encoded by Prokaryotic essential gene #5459.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
Query Match           6.0%;    Score 72; DB 6; Length 396;
Best Local Similarity 21.6%;   Pred. No. 43;
RESULT 1062
ID  ABG25051 standard; protein; 414 AA.
DE  Novel human diagnostic protein.
PN  WO200175067-A2.
PD  11-OCT-2001.
PA  (HYSB-) HYSEQ INC.
Query Match           6.0%;    Score 72; DB 4; Length 414;
Best Local Similarity 22.6%;   Pred. No. 46;
RESULT 1063
ID  AAG50203 standard; protein; 427 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 63592.
PN  EP1033405-A2.
PD  06-SEP-2000.
Query Match           6.0%;    Score 72; DB 3; Length 427;
Best Local Similarity 22.0%;   Pred. No. 48;

RESULT 1064
ID  AAG50202 standard; protein; 430 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 63591.
PN  EP1033405-A2.
PD  06-SEP-2000.
Query Match           6.0%;    Score 72; DB 3; Length 430;
Best Local Similarity 22.0%;   Pred. No. 49;
RESULT 1065
ID  ABM72825 standard; protein; 447 AA.
DE  Staphylococcus aureus protein #2065.
PN  WO200294868-A2.
PD  28-NOV-2002.
PA  (CHIR-) CHIRON SPA.
Query Match           6.0%;    Score 72; DB 6; Length 447;
Best Local Similarity 23.9%;   Pred. No. 51;
RESULT 1066
ID  ABB62902 standard; protein; 448 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 15498.
PN  WO200171042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
Query Match           6.0%;    Score 72; DB 4; Length 448;
Best Local Similarity 25.1%;   Pred. No. 52;
RESULT 1067
ID  ABJ18913 standard; protein; 453 AA.
DE  Pathogen specific antigen related staphylococcal protein SEQ ID No 59.
PN  WO200259148-A2.
PD  01-AUG-2002.
PA  (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match           6.0%;    Score 72; DB 6; Length 453;
Best Local Similarity 23.9%;   Pred. No. 52;
RESULT 1068
ID  ABU16441 standard; protein; 453 AA.
DE  Protein encoded by Prokaryotic essential gene #1968.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
Query Match           6.0%;    Score 72; DB 6; Length 453;
Best Local Similarity 23.9%;   Pred. No. 52;
RESULT 1069
ID  ADN73057 standard; protein; 468 AA.
DE  Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 952.
PN  WO2004035798-A2.
PD  29-APR-2004.
PA  (CROP-) CROPDESIGN NV.
Query Match           6.0%;    Score 72; DB 8; Length 468;
Best Local Similarity 21.8%;   Pred. No. 55;
RESULT 1070
ID  AAG16338 standard; protein; 495 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 16945.
PN  EP1033405-A2.
PD  06-SEP-2000.
Query Match           6.0%;    Score 72; DB 3; Length 495;
Best Local Similarity 21.8%;   Pred. No. 59;
RESULT 1071
ID  AAG16337 standard; protein; 497 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 16944.
PN  EP1033405-A2.
PD  06-SEP-2000.
Query Match           6.0%;    Score 72; DB 8; Length 497;
Best Local Similarity 21.3%;   Pred. No. 60;
RESULT 1072
ID  AED61108 standard; protein; 497 AA.
DE  Thale cress protein #81.
PN  US20052467858-A1.
PD  03-NOV-2005.
PA  (CERE-) CERES INC.
Query Match           6.0%;    Score 72; DB 3; Length 497;
Best Local Similarity 21.3%;   Pred. No. 60;
RESULT 1073
ID  AEF26566 standard; protein; 497 AA.
DE  A. thaliana cytochrome P450 homolog SEQ ID NO: 85.
PN  US2006015970-A1.
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PD   19-JAN-2006.
PA   (CERS-) CERS INC.
Query Match        6.0%;  Score 72;  DB 10;  Length 497;
Best Local Similarity  21.3%;  Pred. No. 60;

RESULT 1074
ID   AAG16336 standard; protein; 507 AA.
PN   EP1033405-A2.
PD   06-SEP-2000.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 16943.
Query Match        6.0%;  Score 72;  DB 3;  Length 507;
Best Local Similarity  21.3%;  Pred. No. 61;

RESULT 1075
ID   ADS23568 standard; protein; 543 AA.
PN   US2003233675-A1.
PD   18-DEC-2003.
DE   Bacterial polypeptide #12601.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match        6.0%;  Score 72;  DB 8;  Length 543;
Best Local Similarity  18.6%;  Pred. No. 67;

RESULT 1076
ID   ABU25738 standard; protein; 552 AA.
PN   WO200277183-A2.
PD   03-OCT-2002.
DE   Protein encoded by Prokaryotic essential gene #11265.
PA   (ELIT-) ELITRA PHARM INC.
Query Match        6.0%;  Score 72;  DB 6;  Length 552;
Best Local Similarity  19.5%;  Pred. No. 69;

RESULT 1077
ID   AAG50201 standard; protein; 556 AA.
PN   EP1033405-A2.
PD   06-SEP-2000.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63590.
Query Match        6.0%;  Score 72;  DB 3;  Length 556;
Best Local Similarity  22.0%;  Pred. No. 70;

RESULT 1078
ID   ADJ69383 standard; protein; 594 AA.
PN   WO200308768-A2.
PD   23-OCT-2003.
DE   Human heat mitochondrial protein as a therapeutic target SeqID1189.
PA   (BUCK-) BUCK INST AGE RES.
PA   (MITO-) MITOKOR.
Query Match        6.0%;  Score 72;  DB 7;  Length 594;
Best Local Similarity  20.8%;  Pred. No. 76;

RESULT 1079
ID   ABB97202 standard; protein; 696 AA.
PN   WO2003024392-A2.
PD   27-MAR-2003.
DE   Tumour-associated antigenic target protein TAT247 SEQ ID NO:84.
PA   (GETH ) GENENTECH INC.
Query Match        6.0%;  Score 72;  DB 6;  Length 696;
Best Local Similarity  20.8%;  Pred. No. 95;

RESULT 1080
ID   ABP97201 standard; protein; 696 AA.
PN   WO2003024392-A2.
PD   27-MAR-2003.
DE   Tumour-associated antigenic target protein TAT225 SEQ ID NO:83.
PA   (GETH ) GENENTECH INC.
Query Match        6.0%;  Score 72;  DB 6;  Length 696;
Best Local Similarity  20.8%;  Pred. No. 95;

RESULT 1081
ID   ABP81969 standard; protein; 696 AA.
PN   WO2002061087-A2.
PD   08-AUG-2002.
DE   Human GPCR XPR1 protein SEQ ID NO:424.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match        6.0%;  Score 72;  DB 6;  Length 696;
Best Local Similarity  20.8%;  Pred. No. 95;

RESULT 1082
ID   ADB67652 standard; protein; 696 AA.
DE   Human xenotropic& polytropic retrovirus receptor, SEQ ID 21.
PN   WO2003072824-A1.
PD   04-SEP-2003.
PA   (SANY ) SANKYO CO LTD.
Query Match        6.0%;  Score 72;  DB 7;  Length 696;
Best Local Similarity  20.8%;  Pred. No. 95;

RESULT 1083
ID   ADQ96380 standard; protein; 696 AA.
DE   T cell activation associated protein #279.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match        6.0%;  Score 72;  DB 8;  Length 696;
Best Local Similarity  21.3%;  Pred. No. 95;

RESULT 1084
ID   ABM69179 standard; protein; 724 AA.
DE   Photorhabdus luminescens protein sequence #2276.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
Query Match        6.0%;  Score 72;  DB 6;  Length 724;
Best Local Similarity  21.3%;  Pred. No. 1e+02;

RESULT 1085
ID   AAB46702 standard; protein; 741 AA.
DE   P. falciparum DNA polymerase protein fragment SEQ ID NO 11.
PN   WO200075335-A2.
PD   14-DEC-2000.
PA   (DECO-) DECODE GENETICS EHF.
Query Match        6.0%;  Score 72;  DB 4;  Length 741;
Best Local Similarity  30.4%;  Pred. No. 1e+02;

RESULT 1086
ID   AAM47977 standard; protein; 788 AA.
DE   Human hARRG.
PN   CN1315342-A.
PD   03-OCT-2001.
PA   (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
Query Match        6.0%;  Score 72;  DB 5;  Length 788;
Best Local Similarity  26.3%;  Pred. No. 1.1e+02;

RESULT 1087
ID   ABB58917 standard; protein; 1275 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 3543.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Query Match        6.0%;  Score 72;  DB 3;  Length 1275;
Best Local Similarity  19.0%;  Pred. No. 2.2e+02;

RESULT 1088
ID   AAY70064 standard; protein; 2307 AA.
DE   Recombinant fusion pHCAP-1 polyprotein.
PN   WO200008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
Query Match        6.0%;  Score 72;  DB 3;  Length 2307;
Best Local Similarity  23.6%;  Pred. No. 5e+02;

RESULT 1089
ID   AAY70065 standard; protein; 2307 AA.
DE   Recombinant fusion pHCAP-3 polyprotein.
PN   WO200008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
Query Match        6.0%;  Score 72;  DB 3;  Length 2307;
Best Local Similarity  23.6%;  Pred. No. 5e+02;

RESULT 1090
ID   AAY70066 standard; protein; 2307 AA.
DE   Recombinant fusion pHCAP-4 polyprotein.
PN   WO200008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
Query Match        6.0%;  Score 72;  DB 3;  Length 2307;
Best Local Similarity  23.6%;  Pred. No. 5e+02;

RESULT 1091
ID   AAM93791 standard; protein; 208 AA.

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DE   Human polypeptide, SEQ ID NO: 3817.
PD
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 25.2%; Score 71.5; DB 4; Length 208; Pred. No. 20;

RESULT 1092
ID   ADL31784 standard; protein; 208 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3817.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 25.6%; Score 71.5; DB 8; Length 208; Pred. No. 20;

RESULT 1093
ID   AAG56417 standard; protein; 209 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 72517.
PN   EP1033405-A2.
PD   06-SEP-2000.
Query Match
Best Local Similarity 25.6%; Score 71.5; DB 3; Length 209; Pred. No. 21;

RESULT 1094
ID   AAG56416 standard; protein; 216 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 72516.
PN   EP1033405-A2.
PD   06-SEP-2000.
Query Match
Best Local Similarity 25.6%; Score 71.5; DB 3; Length 216; Pred. No. 21;

RESULT 1095
ID   AAG16922 standard; protein; 218 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 17750.
PN   EP1033405-A2.
PD   06-SEP-2000.
Query Match
Best Local Similarity 42.4%; Score 71.5; DB 3; Length 218; Pred. No. 21;

RESULT 1096
ID   ABB53486 standard; protein; 301 AA.
DE   Lactococcus lactis protein ybiG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 26.5%; Score 71.5; DB 5; Length 301; Pred. No. 22;

RESULT 1097
ID   AAW37976 standard; protein; 342 AA.
DE   Kaposi's sarcoma associated herpesvirus G protein-coupled receptor.
PN   WO9815289-A1.
PD   16-APR-1998.
PA   (CORR ) CORNELL RES FOUND INC.
Query Match
Best Local Similarity 22.2%; Score 71.5; DB 2; Length 342; Pred. No. 34;

RESULT 1098
ID   ADG87423 standard; protein; 348 AA.
DE   Meloidogyne incognita plk1 protein.
PN   US2003150017-A1.
PD   07-AUG-2003.
PA   (MESA-) MESA J R B.
PA   (GRAH/) GRAHAM M W.
PA   (FAIR/) FAIRBAIRN D J.
Query Match
Best Local Similarity 21.0%; Score 71.5; DB 7; Length 348; Pred. No. 41;

RESULT 1099
ID   AEF77681 standard; protein; 362 AA.
DE   Rat prostaglandin E receptor 2 (PTGER2).
PN   WO200601171-A2.
PD   16-FEB-2006.
PA   (META-) METABOLEX INC.
Query Match
Best Local Similarity 24.3%; Score 71.5; DB 10; Length 362; Pred. No. 42;

RESULT 1100
ID   ADR40542 standard; protein; 363 AA.
DE   Ovine MlA protein.
PN   US2004161823-A1.
PD   19-AUG-2004.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
PA   (HAWK/) HAWKEN D R.
Query Match
Best Local Similarity 23.1%; Score 71.5; DB 8; Length 363; Pred. No. 44;

RESULT 1101
ID   AAR88410 standard; protein; 366 AA.
DE   High-affinity melatonin-1a receptor.
PN   WO9555320-A1.
PD   28-DEC-1995.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match
Best Local Similarity 23.1%; Score 71.5; DB 2; Length 366; Pred. No. 45;

RESULT 1102
ID   ABU00809 standard; protein; 382 AA.
DE   Angiogenesis-associated human protein sequence #1.
PN   WO200279492-A2.
PD   10-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 22.3%; Score 71.5; DB 6; Length 382; Pred. No. 47;

RESULT 1103
ID   ABP58069 standard; protein; 382 AA.
DE   Human G-protein coupled receptor GAVE1.
PN   WO200295056-A2.
PD   28-NOV-2002.
PA   (AVET ) AVENTIS PHARM INC.
Query Match
Best Local Similarity 22.3%; Score 71.5; DB 6; Length 382; Pred. No. 47;

RESULT 1104
ID   ABP59277 standard; protein; 382 AA.
DE   Human Edg1 receptor.
PN   WO2003006503-A1.
PD   23-JAN-2003.
PA   (CERE-) CERETEK.
Query Match
Best Local Similarity 22.3%; Score 71.5; DB 6; Length 382; Pred. No. 47;

RESULT 1105
ID   ABU08809 standard; protein; 382 AA.
DE   Human EDG-1 protein.
PN   US2002155512-A1.
PD   24-OCT-2002.
PA   (RIGE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 22.3%; Score 71.5; DB 6; Length 382; Pred. No. 47;

RESULT 1106
ID   ABR59701 standard; protein; 382 AA.
DE   Human endothelial differentiation sphingolipid GPCR 1.
PN   WO2003029277-A2.
PD   10-APR-2003.
PA   (RIGE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 22.3%; Score 71.5; DB 6; Length 382; Pred. No. 47;

RESULT 1107
ID   ABP81876 standard; protein; 382 AA.
DE   Human sphingolipid receptor Edg1 protein SEQ ID NO:237.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity 22.3%; Score 71.5; DB 6; Length 382; Pred. No. 47;

RESULT 1108
ID   ADB67662 standard; protein; 382 AA.
DE   Human EDG1, SEQ ID 31.
PN   WO2003072824-A1.
PD   04-SEP-2003.
PA   (SANY ) SANKYO CO LTD.
Query Match
Best Local Similarity 22.3%; Score 71.5; DB 7; Length 382; Pred. No. 47;

RESULT 1109
ID   ADC40477 standard; protein; 382 AA.
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DE   Protein of human EDG-1.
PN   WO2003052096-A1.
PD   26-JUN-2003.
PA   (TAKE ) TAKEDA CHEM IND LTD.
  Query Match
  Best Local Similarity   22.3%;  Score 71.5;  DB 7;  Length 382;

RESULT 1110
ID   ADN38684 standard; protein; 382 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:2.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PD   12-SEP-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
  Query Match
  Best Local Similarity   22.3%;  Score 71.5;  DB 7;  Length 382;

RESULT 1111
ID   ABM85457 standard; protein; 382 AA.
DE   Human protein sequence hCP1630135.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
  Query Match
  Best Local Similarity   22.3%;  Score 71.5;  DB 7;  Length 382;

RESULT 1112
ID   ADJ45541 standard; protein; 382 AA.
DE   LXR-ligand induced transcript seq id 72.
PN   US2004023276-A1.
PD   05-FEB-2004.
PA   (WARD/) WARD T R.
PA   (MAOM/) MAO M.
PA   (LINS/) LINSLEY P S.
PA   (LUND/) LUND E.
  Query Match
  Best Local Similarity   22.3%;  Score 71.5;  DB 8;  Length 382;

RESULT 1113
ID   ADR67022 standard; protein; 382 AA.
DE   Human cancer associated protein sequence SEQ ID NO:68.
PN   WO2004074321-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
  Query Match
  Best Local Similarity   22.3%;  Score 71.5;  DB 8;  Length 382;

RESULT 1114
ID   ADY19566 standard; protein; 382 AA.
DE   PRO polypeptide SEQ ID NO 5372.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity   22.3%;  Score 71.5;  DB 8;  Length 382;

RESULT 1115
ID   ADZ12975 standard; protein; 382 AA.
DE   Human cancer-associated protein #147.
PN   WO2005031001-A2.
PD   07-APR-2005.
PA   (CHIR ) CHIRON CORP.
  Query Match
  Best Local Similarity   22.3%;  Score 71.5;  DB 9;  Length 382;

RESULT 1116
ID   ADZ12973 standard; protein; 382 AA.
DE   Human cancer-associated protein #146.
PN   WO2005031001-A2.
PD   07-APR-2005.
PA   (CHIR ) CHIRON CORP.
  Query Match
  Best Local Similarity   22.3%;  Score 71.5;  DB 9;  Length 382;

RESULT 1117
ID   ADN19614 standard; protein; 383 AA.
DE   Bacterial polypeptide #2267.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match
  Best Local Similarity   22.3%;  Score 71.5;  DB 9;  Length 383;

RESULT 1118
ID   ABB05226 standard; protein; 390 AA.
DE   Catostomus commersoni isotocin receptor protein SEQ ID NO:3.
PN   WO200192296-A2.
PD   06-DEC-2001.
PA   (FARB ) BAYER AG.
  Query Match
  Best Local Similarity   22.2%;  Score 71.5;  DB 5;  Length 390;

RESULT 1119
ID   ADM83141 standard; protein; 394 AA.
DE   Rat vesicle membrane protein (VMP)2.
PN   US2003175787-A1.
PD   18-SEP-2003.
PA   (INCY-) INCYTE CORP.
  Query Match
  Best Local Similarity   22.7%;  Score 71.5;  DB 7;  Length 394;

RESULT 1120
ID   ABB48023 standard; protein; 435 AA.
DE   Listeria monocytogenes protein #727.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP ) INST PASTEUR.
  Query Match
  Best Local Similarity   21.4%;  Score 71.5;  DB 5;  Length 435;

RESULT 1121
ID   AAR22000 standard; protein; 441 AA.
DE   Partial M17 antigen from Region II, encoded by PCR prod.
PN   WO9203457-A.
PD   05-MAR-1992.
PA   (REGC ) UNIV CALIFORNIA.
  Query Match
  Best Local Similarity   22.6%;  Score 71.5;  DB 2;  Length 441;

RESULT 1122
ID   ADX93096 standard; protein; 448 AA.
DE   Plant full length insert polypeptide seqid 55760.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (ZHOU/) ZHOU Y.
PA   (LIUJ/) LIU J.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
  Query Match
  Best Local Similarity   22.3%;  Score 71.5;  DB 8;  Length 448;

RESULT 1123
ID   ABP75877 standard; protein; 470 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 1061.
PN   WO200283876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match
  Best Local Similarity   22.3%;  Score 71.5;  DB 6;  Length 470;

RESULT 1124
ID   ABU26033 standard; protein; 524 AA.
DE   Protein encoded by Prokaryotic essential gene #11560.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
  Query Match
  Best Local Similarity   22.4%;  Score 71.5;  DB 6;  Length 524;

RESULT 1125
ID   ABJ37074 standard; protein; 565 AA.
DE   Human breast cancer / ovarian cancer related protein #50.
PN   WO2003000012-A2.
PD   03-JAN-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match
  Best Local Similarity   22.4%;  Score 71.5;  DB 6;  Length 565;
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RESULT 1126
ID   AAW51244 standard; protein; 568 AA.
DE   Human calcitonin receptor.
PN   WO9821242-A1.
PD   22-MAY-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match
     Best Local Similarity   22.4%;   Score 71.5;   DB 2;   Length 568;

RESULT 1127
ID   ABU16392 standard; protein; 603 AA.
DE   Protein encoded by Prokaryotic essential gene #1919.
PN   WO20277183-A2.
PD   03-OCT-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match
     Best Local Similarity   21.3%;   Score 71.5;   DB 6;   Length 603;

RESULT 1128
ID   ABM72619 standard; protein; 603 AA.
DE   Staphylococcus aureus protein #1859.
PN   WO20294868-A2.
PD   28-NOV-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match
     Best Local Similarity   21.3%;   Score 71.5;   DB 6;   Length 603;

RESULT 1129
ID   AEC46140 standard; protein; 689 AA.
DE   Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 48.
PN   US20051191701-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match
     Best Local Similarity   22.8%;   Score 71.5;   DB 9;   Length 689;

RESULT 1130
ID   ADM43215 standard; protein; 697 AA.
DE   Human methionine synthase reductase del Arg 559 variant.
PN   US20030832676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match
     Best Local Similarity   22.8%;   Score 71.5;   DB 7;   Length 697;

RESULT 1131
ID   ADM43217 standard; protein; 697 AA.
DE   Human methionine synthase reductase del Leu 576 variant.
PN   US20030832676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match
     Best Local Similarity   22.8%;   Score 71.5;   DB 7;   Length 697;

RESULT 1132
ID   AEC46138 standard; protein; 697 AA.
DE   Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 46.
PN   US20051191701-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match
     Best Local Similarity   22.8%;   Score 71.5;   DB 9;   Length 697;

RESULT 1133


RESULT 1134
ID   AAB07591 standard; protein; 698 AA.
DE   A human methionine synthase reductase polypeptide.
PN   WO20042196-A2.
PD   20-JUL-2000.
PA   (UTMC-) UNIV MCGILL.
     Query Match
     Best Local Similarity   22.8%;   Score 71.5;   DB 3;   Length 698;

RESULT 1135
ID   ABG00883 standard; protein; 698 AA.
DE   Novel human diagnostic protein #874.
PN   WO20175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match
     Best Local Similarity   22.8%;   Score 71.5;   DB 4;   Length 698;

RESULT 1136
ID   ADM43211 standard; protein; 698 AA.
DE   Human methionine synthase reductase Met22Ile variant.
PN   US20030832676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match
     Best Local Similarity   22.8%;   Score 71.5;   DB 7;   Length 698;

RESULT 1137
ID   ADM43213 standard; protein; 698 AA.
DE   Human methionine synthase reductase Cys37Tyr variant.
PN   US20030832676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match
     Best Local Similarity   22.8%;   Score 71.5;   DB 7;   Length 698;

RESULT 1138
ID   ADM43207 standard; protein; 698 AA.
DE   Human wild-type methionine synthase reductase.
PN   US20030832676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match
     Best Local Similarity   22.8%;   Score 71.5;   DB 7;   Length 698;

RESULT 1139
ID   ADQ39857 standard; protein; 698 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1520.
PN   WO20040580S2-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match
     Best Local Similarity   22.8%;   Score 71.5;   DB 8;   Length 698;

RESULT 1140
ID   AEC46136 standard; protein; 698 AA.
DE   Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 44.
PN   US20051191701-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match
     Best Local Similarity   22.8%;   Score 71.5;   DB 9;   Length 698;

ID   AEC46113 standard; protein; 698 AA.
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DE   Human methionine synthase reductase (MTRR) protein, SEQ ID NO: 21.
PN   US2005191701-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R. A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
RESULT 1141
  Query Match             6.0%;   Score 71.5;   DB 9;   Length 698;
  Best Local Similarity  22.8%;   Pred. No. 1.1e+02;

ID   AEC46134 standard; protein; 698 AA.
DE   Human methionine synthase reductase (MTRR) protein, SEQ ID NO: 42.
PN   US2005191701-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R. A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
RESULT 1142
  Query Match             6.0%;   Score 71.5;   DB 9;   Length 698;
  Best Local Similarity  22.8%;   Pred. No. 1.1e+02;

ID   AEC46094 standard; protein; 698 AA.
DE   Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 2.
PN   US2005191701-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R. A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
RESULT 1143
  Query Match             6.0%;   Score 71.5;   DB 9;   Length 698;
  Best Local Similarity  22.8%;   Pred. No. 1.1e+02;

ID   ADQ39858 standard; protein; 725 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1521.
PN   WO2004050852-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
RESULT 1144
  Query Match             6.0%;   Score 71.5;   DB 8;   Length 725;
  Best Local Similarity  22.8%;   Pred. No. 1.2e+02;

ID   ADU06586 standard; protein; 725 AA.
DE   Novel bronchial cancer-associated human protein SeqID812.
PN   DE10316701-A1.
PD   04-NOV-2004.
PA   (HINZ/) HINZMANN B.
PA   (HERM/) HERMANN K.
PA   (CAST/) HEIDEN CASTANOS-VELEZ E.
RESULT 1145
  Query Match             6.0%;   Score 71.5;   DB 8;   Length 725;
  Best Local Similarity  22.8%;   Pred. No. 1.2e+02;

ID   AAY51606 standard; protein; 890 AA.
DE   Human wml protein.
PN   DE19845277-C1.
PD   09-MAR-2000.
PA   (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
RESULT 1146
  Query Match             6.0%;   Score 71.5;   DB 5;   Length 890;
  Best Local Similarity  23.8%;   Pred. No. 1.5e+02;

ID   ABB78282 standard; protein; 890 AA.
DE   Amino acid sequence of human wolframin polypeptide.
PN   WO200263307-A2.
PD   15-AUG-2002.
PA   (PHAA ) PHARMACIA & UPJOHN CO.
RESULT 1147
  Query Match             6.0%;   Score 71.5;   DB 6;   Length 890;
  Best Local Similarity  23.8%;   Pred. No. 1.5e+02;

ID   ADD46013 standard; protein; 890 AA.
DE   Human Protein O76024, SEQ ID NO 11685.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
RESULT 1148
  Query Match             6.0%;   Score 71.5;   DB 7;   Length 890;
  Best Local Similarity  23.8%;   Pred. No. 1.5e+02;

ID   ADF69127 standard; protein; 890 AA.
DE   Human MP53 protein sequence SEQ ID NO:97.
PN   WO2003083047-A2.
PD   17-MAR-2005.
PA   (EXEL-) EXELIXIS INC.
PD   09-OCT-2003.
RESULT 1149
  Query Match             6.0%;   Score 71.5;   DB 7;   Length 890;
  Best Local Similarity  23.8%;   Pred. No. 1.5e+02;

ID   ADY70426 standard; protein; 890 AA.
DE   Human beta-amyloid precursor protein, wolframin.
PN   WO2005023858-A1.
PD   17-MAR-2005.
PA   (CELL-) CELLZOME AG.
RESULT 1150
  Query Match             6.0%;   Score 71.5;   DB 9;   Length 890;
  Best Local Similarity  23.8%;   Pred. No. 1.5e+02;

ID   ADY70680 standard; protein; 890 AA.
DE   Human nicastrin/Psen2-complex member, wolframin protein.
PN   WO2005023833-A2.
PD   17-MAR-2005.
PA   (CELL-) CELLZOME AG.
RESULT 1151
  Query Match             6.0%;   Score 71.5;   DB 9;   Length 890;
  Best Local Similarity  23.8%;   Pred. No. 1.5e+02;

ID   AEE39892 standard; protein; 890 AA.
DE   Amino acid sequence SEQ ID NO:24.
PN   WO2005112978-A2.
PD   01-DEC-2005.
PA   (UTAH ) UNIV UTAH RES FOUND.
RESULT 1152
  Query Match             6.0%;   Score 71.5;   DB 10;   Length 890;
  Best Local Similarity  23.8%;   Pred. No. 1.5e+02;

ID   ADI22689 standard; protein; 2245 AA.
DE   Human disease detection and treatment (MDDT) protein - SEQ ID 138.
PN   WO2003062379-A2.
PD   31-JUL-2003.
PA   (INCY-) INCYTE GENOMICS INC.
RESULT 1153
  Query Match             6.0%;   Score 71.5;   DB 7;   Length 2245;
  Best Local Similarity  23.8%;   Pred. No. 5.5e+02;

ID   AAB42192 standard; protein; 2405 AA.
DE   Human ORFX ORF1956 polypeptide sequence SEQ ID NO:3912.
PN   WO200058473-A2.
PD   05-OCT-2000.
PA   (CURA-) CURAGEN CORP.
RESULT 1154
  Query Match             6.0%;   Score 71.5;   DB 3;   Length 2405;
  Best Local Similarity  22.4%;   Pred. No. 6.1e+02;

ID   ABB11404 standard; protein; 2560 AA.
DE   Human FLAMINGO 1 homologue, SEQ ID NO:1774.
PN   WO200157188-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
RESULT 1155
  Query Match             6.0%;   Score 71.5;   DB 4;   Length 2560;
  Best Local Similarity  22.4%;   Pred. No. 6.6e+02;

ID   ABU11556 standard; peptide; 2894 AA.
DE   Human MDDT polypeptide SEQ ID 503.
PN   WO200279449-A2.
PD   10-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
RESULT 1156
  Query Match             6.0%;   Score 71.5;   DB 6;   Length 2894;
  Best Local Similarity  22.4%;   Pred. No. 7.9e+02;

ID   AAU07054 standard; protein; 2923 AA.
DE   Human Flamingo protein encoded by cDNA splice variant.
PN   WO200161003-A1.
PD   23-AUG-2001.

PA   (SMIK ) SMITHKLINE BEECHAM PLC.
Query Match            6.0%;  Score 71.5;  DB 4;  Length 2923;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1157
ID   AAM50866 standard; protein; 2923 AA.
DE   Cadherin EGF LAG seven-pass G-type receptor 2, basal cell marker.
PN   WO020208765-A2.
PD   31-JAN-2002.
PA   (STRD ) UNIV. STANFORD.
PA   (GENO-) APPLIED GENOMICS INC.
Query Match            6.0%;  Score 71.5;  DB 5;  Length 2923;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1158
ID   ABP82018 standard; protein; 2923 AA.
DE   Human GPCR CELSR2 protein SEQ ID NO:524.
PN   WO020261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match            6.0%;  Score 71.5;  DB 6;  Length 2923;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1159
ID   ADC15499 standard; protein; 2923 AA.
DE   Human cadherin EGF LAG seven-pass G-type receptor 2.
PN   US20030086934-A1.
PD   08-MAY-2003.
PA   (BOTS/) BOTSTEIN D.
PA   (BROW/) BROWN P O.
PA   (PERO/) PEROU C M.
PA   (RING/) RING B.
PA   (ROSS/) ROSS D.
PA   (SEIT/) SEITZ R.
PA   (VRIJ/) VAN DE RIJN J M.
Query Match            6.0%;  Score 71.5;  DB 7;  Length 2923;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1160
ID   ADC86479 standard; protein; 2923 AA.
DE   Human GPCR protein SEQ ID NO:932.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match            6.0%;  Score 71.5;  DB 7;  Length 2923;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1161
ID   ADE54407 standard; protein; 2923 AA.
DE   Human Protein XP_042739, SEQ ID NO 210.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
Query Match            6.0%;  Score 71.5;  DB 7;  Length 2923;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1162
ID   ADE54411 standard; protein; 2923 AA.
DE   Human Protein XP_042739, SEQ ID NO:346.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
Query Match            6.0%;  Score 71.5;  DB 8;  Length 2923;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1163
ID   ADQ29245 standard; protein; 2923 AA.
DE   Human GPCR CELSR2, SEQ ID NO.346.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
Query Match            6.0%;  Score 71.5;  DB 8;  Length 2923;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1164
ID   ADY70314 standard; protein; 2923 AA.
DE   Human beta-APP, cadherin EGF LAG seven-pass G-type receptor 2.
PN   WO2005023858-A1.

PD   17-MAR-2005.
PA   (CELL-) CELLZOME AG.
Query Match            6.0%;  Score 71.5;  DB 9;  Length 2923;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1165
ID   ADY70652 standard; protein; 2923 AA.
DE   Human BACE1/PTK7-complex member, CELSR2 protein.
PN   WO2005023833-A2.
PD   17-MAR-2005.
PA   (CELL-) CELLZOME AG.
Query Match            6.0%;  Score 71.5;  DB 9;  Length 2923;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1166
ID   ADY70648 standard; protein; 2923 AA.
DE   Human BACE1-complex, cadherin seven-pass G-type receptor 2 protein.
PN   WO2005023833-A2.
PD   17-MAR-2005.
PA   (CELL-) CELLZOME AG.
Query Match            6.0%;  Score 71.5;  DB 5;  Length 2936;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1167
ID   AAU74826 standard; protein; 2936 AA.
DE   Human REPTR 9 protein.
PN   WO200198354-A2.
PD   27-DEC-2001.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match            6.0%;  Score 71.5;  DB 9;  Length 2936;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1168
ID   AAU07053 standard; protein; 2956 AA.
DE   Human Flamingo polypeptide.
PN   WO200161003-A1.
PD   23-AUG-2001.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
Query Match            6.0%;  Score 71.5;  DB 9;  Length 2956;
  Best Local Similarity 22.4%;  Pred. No. 8e+02;
RESULT 1169
ID   ADX40788 standard; protein; 3010 AA.
DE   HCV polymerase protein #11.
PN   WO2005012502-A2.
PD   10-FEB-2005.
PA   (EP1M-) EPIMMUNE INC.
Query Match            6.0%;  Score 71.5;  DB 4;  Length 3010;
  Best Local Similarity 22.4%;  Pred. No. 8.1e+02;
RESULT 1170
ID   AAR34468 standard; protein; 3011 AA.
DE   Encoded by full-length Hepatitis C virus clone JK1-B.
PN   JP05068562-A.
PD   23-MAR-1993.
PA   (SANW ) SANWA KAGAKU KENKYUSHO CO.
Query Match            6.0%;  Score 71.5;  DB 2;  Length 3011;
  Best Local Similarity 23.7%;  Pred. No. 8.3e+02;
RESULT 1171
ID   AAR31621 standard; protein; 3011 AA.
DE   Hepatitis C virus (HCV) polyprotein.
PN   WO930365-A2.
PD   07-JAN-1993.
PA   (CHIR ) CHIRON CORP.
Query Match            6.0%;  Score 71.5;  DB 2;  Length 3011;
  Best Local Similarity 22.8%;  Pred. No. 8.3e+02;
RESULT 1172
ID   ABB67866. standard; protein; 5303 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 30390.
PN   WO2001171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Query Match            6.0%;  Score 71.5;  DB 4;  Length 5303;
  Best Local Similarity 29.5%;  Pred. No. 1.8e+03;
RESULT 1173
ID   AEF50785 standard; protein; 195 AA.
DE   MmusC A8 clone, hypothetical transmembrane protein #1.
PN   WO200605943-A1.
PD   19-JAN-2006.

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PA   (MORE-) MOREDUN RES INST.
Query Match             5.9%;  Score 71;  DB 10;  Length 195;
Best Local Similarity  25.0%;  Pred. No. 21;
RESULT 1174
ID   ABB06793 standard; protein; 198 AA.
DE   Human transmembrane 4 protein 22 SEQ ID NO:2.
PN   CN127990-A.
PD   26-DEC-2001.
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match            24.5%;  Score 71;  DB 5;  Length 198;
Best Local Similarity  19.7%;  Pred. No. 22;
RESULT 1175
ID   ABC21170 standard; protein; 217 AA.
DE   L. acidophilus metal-dependent membrane protease #6.
PN   WO2005081959-A2.
PD   09-SEP-2005.
PA   (UTNC-) UNIV NORTH CAROLINA STATE.
Query Match             5.9%;  Score 71;  DB 9;  Length 217;
Best Local Similarity  22.4%;  Pred. No. 25;
RESULT 1176
ID   ADU08919 standard; protein; 223 AA.
DE   Coronavirus membrane protein seqid 42.
PN   WO2004096842-A2.
PD   11-NOV-2004.
PA   (BCCA-) BC CANCER AGENCY.
Query Match             5.9%;  Score 71;  DB 6;  Length 223;
Best Local Similarity  18.6%;  Pred. No. 26;
RESULT 1177
ID   ABR58398 standard; protein; 240 AA.
DE   Human NOV17a.
PN   WO2003029423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.
Query Match            22.4%;  Score 71;  DB 8;  Length 240;
Best Local Similarity  18.7%;  Pred. No. 28;
RESULT 1178
ID   ABP26255 standard; protein; 295 AA.
DE   Streptococcus polypeptide SEQ ID NO 1686.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
Query Match             5.9%;  Score 71;  DB 5;  Length 295;
Best Local Similarity  24.9%;  Pred. No. 38;
RESULT 1179
ID   ADX65958 standard; protein; 309 AA.
DE   Plant full length insert polypeptide seqid 36801.
PN   US20040348888-A1.
PD   19-FEB-2004.
PA   (GENO-) INST GENOMIC RES.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
Query Match             5.9%;  Score 71;  DB 6;  Length 309;
Best Local Similarity  18.7%;  Pred. No. 40;
RESULT 1180
ID   AAG72952 standard; protein; 310 AA.
DE   Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA) YEDA RES & DEV CO LTD.
Query Match            22.9%;  Score 71;  DB 4;  Length 310;
Best Local Similarity   5.9%;  Pred. No. 41;
RESULT 1181
ID   AAR48717 standard; protein; 312 AA.
DE   G-protein coupled human interleukin-8 receptor protein.
PN   WO9405695-A1.
PD   17-MAR-1994.
PA   (UTNY ) UNIV NEW YORK STATE.
Query Match             5.9%;  Score 71;  DB 2;  Length 312;
Best Local Similarity  19.7%;  Pred. No. 41;
RESULT 1182
ID   AAW02689 standard; peptide; 312 AA.
DE   G-protein coupled human interleukin-8 receptor.
PN   US5508384-A.
PD   16-APR-1996.
PA   (UTNY ) UNIV NEW YORK STATE.
Query Match             5.9%;  Score 71;  DB 2;  Length 312;
Best Local Similarity  19.7%;  Pred. No. 41;
RESULT 1183
ID   AAG72169 standard; protein; 312 AA.
DE   Human olfactory receptor polypeptide, SEQ ID NO: 1850.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA ) YEDA RES & DEV CO LTD.
Query Match            22.9%;  Score 71;  DB 4;  Length 312;
Best Local Similarity   5.9%;  Pred. No. 41;
RESULT 1184
ID   AAG72377 standard; protein; 312 AA.
DE   Human OR-like polypeptide query sequence, SEQ ID NO: 2058.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA ) YEDA RES & DEV CO LTD.
Query Match             5.9%;  Score 71;  DB 4;  Length 312;
Best Local Similarity  22.9%;  Pred. No. 41;
RESULT 1185
ID   ADY08080 standard; protein; 364 AA.
DE   Plant full length insert polypeptide seqid 63895.
PN   US20040348888-A1.
PD   19-FEB-2004.
PA   (GENO-) INST GENOMIC RES.
PA   (LIU/)  LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
Query Match             5.9%;  Score 71;  DB 8;  Length 364;
Best Local Similarity  18.7%;  Pred. No. 51;
RESULT 1186
ID   AEF93343 standard; protein; 382 AA.
DE   Canis sphingosine-1-phosphate isoform 1 (cS1P1) receptor.
PN   WO2006014802-A2.
PD   09-FEB-2006.
PA   (MERI-) MERCK & CO INC.
Query Match             5.9%;  Score 71;  DB 10;  Length 382;
Best Local Similarity  20.5%;  Pred. No. 54;
RESULT 1187
ID   ABB54394 standard; protein; 391 AA.
DE   Lactococcus lactis protein ykiI.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
Query Match             5.9%;  Score 71;  DB 5;  Length 391;
Best Local Similarity  20.3%;  Pred. No. 56;
RESULT 1188
ID   ABB48413 standard; protein; 423 AA.
DE   Listeria monocytogenes protein #1117.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP ) INST PASTEUR.
Query Match             5.9%;  Score 71;  DB 5;  Length 423;
Best Local Similarity  28.4%;  Pred. No. 62;
RESULT 1189
ID   ADL05302 standard; protein; 423 AA.
DE   M. catarrhalis protein #1068.
PN   US6673910-B1.
PD   06-JAN-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match             5.9%;  Score 71;  DB 8;  Length 423;
Best Local Similarity  38.0%;  Pred. No. 62;
RESULT 1190
Query Match
Best Local Similarity
```

ID   ADJ95142 standard; protein; 444 AA.
DE   Novel NOVX protein sequence #185.
PN   WO2003040325-A2.
PD   15-MAY-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.9%;   Score 71;   DB 7;   Length 444;
     Best Local Similarity   21.0%;   Pred. No. 67;

RESULT 1191
ID   ADJ95144 standard; protein; 444 AA.
DE   Novel NOVX protein sequence #186.
PN   WO2003040325-A2.
PD   15-MAY-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.9%;   Score 71;   DB 7;   Length 444;
     Best Local Similarity   21.0%;   Pred. No. 67;

RESULT 1192
ID   ADU73808 standard; protein; 448 AA.
DE   Drosophila melanogaster Cbl-b.
PN   WO2004099388-A2.
PD   18-NOV-2004.
PA   (PROT-) PROTEOLOGICS INC.
     Query Match   5.9%;   Score 71;   DB 8;   Length 448;
     Best Local Similarity   23.5%;   Pred. No. 68;

RESULT 1193
ID   ADU69155 standard; protein; 448 AA.
DE   Fruit fly CBL-B protein.
PN   WO2004098492-A2.
PD   18-NOV-2004.
PA   (PROT-) PROTEOLOGICS INC.
     Query Match   5.9%;   Score 71;   DB 8;   Length 448;
     Best Local Similarity   23.5%;   Pred. No. 68;

RESULT 1194
ID   ADW87442 standard; protein; 448 AA.
DE   Drosophila melanogaster CBL-B.
PN   WO2005007141-A2.
PD   27-JAN-2005.
PA   (PROT-) PROTEOLOGICS INC.
     Query Match   5.9%;   Score 71;   DB 9;   Length 448;
     Best Local Similarity   23.5%;   Pred. No. 68;

RESULT 1195
ID   ADP29417 standard; protein; 455 AA.
DE   Human secreted protein SEQ ID #1415.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
     Query Match   5.9%;   Score 71;   DB 8;   Length 455;
     Best Local Similarity   24.3%;   Pred. No. 69;

RESULT 1196
ID   ABU19912 standard; protein; 457 AA.
DE   Protein encoded by Prokaryotic essential gene #5439.
PN   WO2002077183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.9%;   Score 71;   DB 6;   Length 457;
     Best Local Similarity   22.0%;   Pred. No. 69;

RESULT 1197
ID   ADI24575 standard; protein; 470 AA.
DE   Human endogenous 5HT2A serotonin receptor.
PN   US2003224442-A1.
PD   04-DEC-2003.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
PA   (LIAW/) LIAW C W.
PA   (RUSS/) RUSSO J F.
PA   (THOM/) THOMSEN W J.
     Query Match   5.9%;   Score 71;   DB 8;   Length 470;
     Best Local Similarity   23.7%;   Pred. No. 72;

RESULT 1198
ID   AAR37659 standard; protein; 471 AA.
DE   Sequence encoded by cDNA.
PN   WO9311257-A2.
PD   10-JUN-1993.
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
     Query Match   5.9%;   Score 71;   DB 2;   Length 471;
     Best Local Similarity   23.7%;   Pred. No. 72;

RESULT 1199
ID   AAW23781 standard; protein; 471 AA.
DE   Human serotonin 5-HT2 receptor protein.
PN   US5561024-A.
PD   26-AUG-1997.
PA   (SYNA-) SYNAPTIC PHARM CORP.
     Query Match   5.9%;   Score 71;   DB 2;   Length 471;
     Best Local Similarity   23.7%;   Pred. No. 72;

RESULT 1200
ID   AAW77107 standard; protein; 471 AA.
DE   Human 5-HT2A serotonin receptor.
PN   WO9938217-A1.
PD   03-SEP-1998.
PA   (HERR/) HERRICK-DAVIS K.
PA   (TEIT/) TEITLER M.
PA   (EGAN/) EGAN C C.
     Query Match   5.9%;   Score 71;   DB 2;   Length 471;
     Best Local Similarity   23.7%;   Pred. No. 72;

RESULT 1201
ID   AAY90640 standard; protein; 471 AA.
DE   Human G protein-coupled receptor 5HT-2A (serotonin receptor).
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%;   Score 71;   DB 3;   Length 471;
     Best Local Similarity   23.7%;   Pred. No. 72;

RESULT 1202
ID   AAY90675 standard; protein; 471 AA.
DE   Human mutant G protein-coupled receptor 5HT-2A.
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%;   Score 71;   DB 3;   Length 471;
     Best Local Similarity   23.7%;   Pred. No. 72;

RESULT 1203
ID   ABB07978 standard; protein; 471 AA.
DE   Human 5-HT2 receptor sequence.
PN   US6383762-B1.
PD   07-MAY-2002.
PA   (SYNA-) SYNAPTIC PHARM CORP.
     Query Match   5.9%;   Score 71;   DB 5;   Length 471;
     Best Local Similarity   23.7%;   Pred. No. 72;

RESULT 1204
ID   ABP81765 standard; protein; 471 AA.
DE   Human 5-HT2A receptor protein SEQ ID NO:12.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match   5.9%;   Score 71;   DB 6;   Length 471;
     Best Local Similarity   23.7%;   Pred. No. 72;

RESULT 1205
ID   ADC22641 standard; protein; 471 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #32.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%;   Score 71;   DB 7;   Length 471;
     Best Local Similarity   23.7%;   Pred. No. 72;

RESULT 1206
ID   ADC22747 standard; protein; 471 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #72.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%;   Score 71;   DB 7;   Length 471;
     Best Local Similarity   23.7%;   Pred. No. 72;

RESULT 1207
ID   ADE65844 standard; protein; 471 AA.
DE   Human serotonin 2A receptor.
PN   US2003170723-A1.
PD   11-SEP-2003.
PA

PA  (SATO/) SATO T.
Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 72;  DB 7;  Length 471;
RESULT 1208
ID  ADH14220 standard; protein; 471 AA.
DE  Mutated human serotonin 5HT_2A.
PN  US2003105292-A1.
PD  05-JUN-2003.
PA  (LIAW/) LIAW C W.
PA  (BEHA/) BEHAN D P.
PA  (CHAL/) CHALMERS D T.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 72;  DB 7;  Length 471;
RESULT 1209
ID  ADH14114 standard; protein; 471 AA.
DE  Human serotonin 5HT_2A.
PN  US2003105292-A1.
PD  05-JUN-2003.
PA  (LIAW/) LIAW C W.
PA  (BEHA/) BEHAN D P.
PA  (CHAL/) CHALMERS D T.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 72;  DB 7;  Length 471;
RESULT 1210
ID  ADL90125 standard; protein; 471 AA.
DE  Human serotonin receptor 5HT2a.
PN  US2003167476-A1.
PD  04-SEP-2003.
PA  (CONK/) CONKLIN B R.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 72;  DB 7;  Length 471;
RESULT 1211
ID  ADO29506 standard; protein; 471 AA.
DE  Human GPCR HTR2A, SEQ ID NO:608.
PN  WO2004040000-A2.
PD  13-MAY-2004.
PA  (PRIM-) PRIMAL INC.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 72;  DB 7;  Length 471;
RESULT 1212
ID  ADO39798 standard; protein; 471 AA.
DE  Human myocardial infarction-associated gene derived protein, SEQ ID 1463.
PN  WO2004058052-A2.
PD  15-JUL-2004.
PA  (APPL-) APPLERA CORP.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 72;  DB 7;  Length 471;
RESULT 1213
ID  ADO39799 standard; protein; 471 AA.
DE  Human myocardial infarction-associated gene derived protein, SEQ ID 1462.
PN  WO2004058052-A2.
PD  15-JUL-2004.
PA  (APPL-) APPLERA CORP.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 72;  DB 8;  Length 471;
RESULT 1214
ID  ADO39800 standard; protein; 471 AA.
DE  Human myocardial infarction-associated gene derived protein, SEQ ID 1461.
PN  WO2004058052-A2.
PD  15-JUL-2004.
PA  (APPL-) APPLERA CORP.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 72;  DB 8;  Length 471;
RESULT 1215
ID  ADU48367 standard; protein; 471 AA.
DE  Human serotonin 2A receptor protein.
PN  US2004229287-A1.
PD  18-NOV-2004.
PA  (UYCO ) UNIV COLUMBIA NEW YORK.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 72;  DB 8;  Length 471;
RESULT 1216
ID  ADX02782 standard; protein; 471 AA.
DE  Human 5-HT 2a receptor protein SeqID22.
PN  WO2005012254-A1.
PD  10-FEB-2005.
PA  (AREN-) ARENA PHARM INC.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 72;  DB 9;  Length 471;
RESULT 1217
ID  ABF70361 standard; protein; 471 AA.
DE  Human 5-hydroxytryptamine 2A receptor protein sequence.
PN  WO2006010515-A2.
PD  02-FEB-2006.
PA  (FARB ) BAYER HEALTHCARE AG.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 72;  DB 10;  Length 471;
RESULT 1218
ID  AAY01626 standard; protein; 478 AA.
DE  Amino acid sequence of the human 5-HT2 receptor.
PN  US5885785-A.
PD  23-MAR-1999.
PA  (SYNA-) SYNAPTIC PHARM CORP.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 74;  DB 2;  Length 478;
RESULT 1219
ID  ABG70577 standard; protein; 480 AA.
DE  Human serotonin (5-HT2) receptor.
PN  US2002009548-A1.
PD  25-JUL-2002.
PA  (SYNA-) SYNAPTIC PHARM CORP.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 74;  DB 5;  Length 480;
RESULT 1220
ID  ABM70440 standard; protein; 493 AA.
DE  Photorhabdus luminescens protein sequence #3537.
PN  WO2002094867-A2.
PD  28-NOV-2002.
PA  (INSP ) INST PASTEUR;
PA  (CNRS ) CNRS CENT NAT RECH SCI.

Query Match                     5.9%;
Best Local Similarity          23.5%;  Score 71;  Pred. No. 77;  DB 6;  Length 493;
RESULT 1221
ID  ADE56383 standard; protein; 545 AA.
DE  Rat Protein O70536, SEQ ID NO 2235.
PN  WO2003016475-A2.
PD  27-FEB-2003.
PA  (GEHO ) GEN HOSPITAL CORP.
PA  (FARB ) BAYER AG.

Query Match                     5.9%;
Best Local Similarity          23.7%;  Score 71;  Pred. No. 89;  DB 7;  Length 545;
RESULT 1222
ID  ADD48660 standard; protein; 545 AA.
DE  Rat Protein BAA25372, SEQ ID NO 14366.
PN  WO2003016475-A2.
PD  27-FEB-2003.
PA  (GEHO ) GEN HOSPITAL CORP.
PA  (FARB ) BAYER AG.

Query Match                     5.9%;
Best Local Similarity          22.0%;  Score 71;  Pred. No. 89;  DB 7;  Length 545;
RESULT 1223
ID  ADS43584 standard; protein; 546 AA.
DE  Bacterial polypeptide #22014.
PN  US2003233675-A1.
PD  18-DEC-2003.
PA  (CAOY/) CAO Y.
PA  (HINK/) HINKLE G J.
PA  (SLAT/) SLATER S C.
PA  (CHEN/) CHEN X.
PA  (GOLD/) GOLDMAN B S.

Query Match                     5.9%;
Best Local Similarity          26.2%;  Score 71;  Pred. No. 89;  DB 8;  Length 546;
RESULT 1224
ID  ABJ26399 standard; protein; 559 AA.
DE  Aspergillus fumigatus essential gene protein #1057.
PN  WO200286090-A2.

PD    31-OCT-2002.
PA    (ELIT-) ELITRA PHARM INC.
Query Match          5.9%;
Best Local Similarity   23.1%;   Score 71;   Pred. No. 92;   DB 6;   Length 559;

RESULT 1225
ID    ABP35686 standard; protein; 563 AA.
DE    Fungal 2BC protein sequence #112.
PN    WO2002024865-A2.
PD    28-MAR-2002.
PA    (MICR-) MICROBIA INC.
Query Match          5.9%;
Best Local Similarity   19.1%;   Score 71;   Pred. No. 93;   DB 5;   Length 563;

RESULT 1226
ID    AAB20578 standard; protein; 564 AA.
DE    Mouse OCTN3 protein SEQ ID NO:1.
PN    WO2004063368-A1.
PD    10-AUG-2000.
PA    (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match          5.9%;
Best Local Similarity   21.4%;   Score 71;   Pred. No. 93;   DB 3;   Length 564;

RESULT 1227
ID    AED51410 standard; protein; 564 AA.
DE    Novel organic cation transporter (OCTN) protein, MOCTN3, SEQ ID NO: 83.
PN    US2005241012-A1.
PD    27-OCT-2005.
PA    (NIGA/) NIGAM S K.
PA    (ERAL/) ERALY S A.
Query Match          5.9%;
Best Local Similarity   21.4%;   Score 71;   Pred. No. 93;   DB 9;   Length 564;

RESULT 1228
ID    AEB36506 standard; protein; 603 AA.
DE    L. pneumophila protein SEQ ID NO 838.
PN    WO2005049642-A2.
PD    02-JUN-2005.
PA    (INSP ) INST PASTEUR.
PA    (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA    (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA    (CNRS ) CNRS CENT NAT RECH SCI.
Query Match          5.9%;
Best Local Similarity   18.3%;   Score 71;   Pred. No. 1e+02;   DB 9;   Length 603;

RESULT 1229
ID    ADQ96374 standard; protein; 631 AA.
DE    T cell activation associated protein #276.
PN    WO2004058805-A2.
PD    15-JUL-2004.
PA    (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match          5.9%;
Best Local Similarity   21.3%;   Score 71;   Pred. No. 1e+02;   DB 8;   Length 631;

RESULT 1230
ID    ADQ96376 standard; protein; 631 AA.
DE    T cell activation associated protein #277.
PN    WO2004058805-A2.
PD    15-JUL-2004.
PA    (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match          5.9%;
Best Local Similarity   21.3%;   Score 71;   Pred. No. 1.1e+02;   DB 8;   Length 631;

RESULT 1231
ID    ABB91532 standard; protein; 676 AA.
DE    Herbicidally active polypeptide SEQ ID NO 743.
PN    WO2002210210-A2.
PD    07-FEB-2002.
PA    (FARB ) BAYER AG.
Query Match          5.9%;
Best Local Similarity   22.3%;   Score 71;   Pred. No. 1.2e+02;   DB 5;   Length 676;

RESULT 1232
ID    AAE21800 standard; protein; 727 AA.
DE    Human HIPHUM 0000029 protein.
PN    GB2365432-A.
PD    20-FEB-2002.
PA    (GLAX ) GLAXO GROUP LTD.
Query Match          5.9%;
Best Local Similarity   24.3%;   Score 71;   Pred. No. 1.3e+02;
RESULT 1233

ID    ABU54636 standard; protein; 727 AA.
DE    Human NOVX polypeptide #95.
PN    WO2002281498-A2.
PD    17-OCT-2002.
PA    (CURA-) CURAGEN CORP.
Query Match          5.9%;
Best Local Similarity   24.3%;   Score 71;   Pred. No. 1.3e+02;   DB 6;   Length 727;

RESULT 1234
ID    ADH76500 standard; protein; 727 AA.
DE    727 amino acid human neurotransmitter transporter protein.
PN    US2003219774-A1.
PD    27-NOV-2003.
PA    (SHAR/) SHARMA R.
PA    (RAMA/) RAMANATHAN C S.
PA    (WEST/) WESTPHAL R.
PA    (FEDE/) FEDER J N.
PA    (LEEL/) LEE L M.
Query Match          5.9%;
Best Local Similarity   24.3%;   Score 71;   Pred. No. 1.3e+02;   DB 8;   Length 727;

RESULT 1235
ID    AEF11189 standard; protein; 742 AA.
DE    HCV protein BP208/FLF SEQ ID NO:44.
PN    WO2006001517-A1.
PD    05-JAN-2006.
PA    (ADIT-) ADVANCED LIFE SCI INST INC.
Query Match          5.9%;
Best Local Similarity   24.8%;   Score 71;   Pred. No. 1.4e+02;   DB 10;   Length 742;

RESULT 1236
ID    ABR62929 standard; protein; 744 AA.
DE    Human neurotransmitter transporter.
PN    WO2003059947-A1.
PD    24-JUL-2003.
PA    (FARB ) BAYER AG.
Query Match          5.9%;
Best Local Similarity   24.8%;   Score 71;   Pred. No. 1.4e+02;   DB 7;   Length 744;

RESULT 1237
ID    ABB60052 standard; protein; 792 AA.
DE    Drosophila melanogaster polypeptide SEQ ID NO 6948.
PN    WO2001171042-A2.
PD    27-SEP-2001.
PA    (PEKE ) PE CORP NY.
Query Match          5.9%;
Best Local Similarity   17.7%;   Score 71;   Pred. No. 1.5e+02;   DB 4;   Length 792;

RESULT 1238
ID    ABM90462 standard; protein; 929 AA.
DE    Rice abiotic stress responsive polypeptide SEQ ID NO:9184.
PN    WO2003008540-A2.
PD    30-JAN-2003.
PA    (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match          5.9%;
Best Local Similarity   20.6%;   Score 71;   Pred. No. 1.9e+02;   DB 7;   Length 929;

RESULT 1239
ID    AAR30616 standard; protein; 3010 AA.
DE    Polypeptide coded by Korean HCV full cDNA sequence LBC1.
PN    EP521318-A2.
PD    07-JAN-1993.
PA    (LUCK-) LUCKY LTD.
Query Match          5.9%;
Best Local Similarity   26.9%;   Score 71;   Pred. No. 9.5e+02;   DB 2;   Length 3010;

RESULT 1240
ID    AAR53417 standard; protein; 3010 AA.
DE    Blood transmissible NANBHV protein.
PN    JP06105690-A.
PD    19-APR-1994.
PA    (KAEN/) KAENNO K.
Query Match          5.9%;
Best Local Similarity   26.9%;   Score 71;   Pred. No. 9.5e+02;   DB 2;   Length 3010;

RESULT 1241
ID    ADX40817 standard; protein; 3010 AA.
DE    HCV polymerase protein #40.
PN    WO2005012502-A2.
PD    10-FEB-2005.
PA    (EPIM-) EPIMMUNE INC.

**RESULT 1242**
ID   ADX40783 standard; protein; 3010 AA.
DE   HCV polymerase protein #6.
PN   WO2005012502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.
Query Match
Best Local Similarity   26.9%;   Score 71;   DB 9;   Length 3010;

**RESULT 1243**
ID   ADX40812 standard; protein; 3010 AA.
DE   HCV polymerase protein #35.
PN   WO2005012502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.
Query Match
Best Local Similarity   26.9%;   Score 71;   Pred. No. 9.5e+02;   Length 3010;

**RESULT 1244**
ID   ABR83573 standard; protein; 202 AA.
DE   BcrC amino acid sequence SEQ ID NO:40.
PN   WO2003057708-A2.
PD   17-JUL-2003.
PA   (EPIM-) EPIMMUNE INC.
Query Match
Best Local Similarity   26.9%;   Score 71;   Pred. No. 9.5e+02;   Length 202;

**RESULT 1245**
ID   AAU01287 standard; protein; 218 AA.
DE   Brassica napus fatty acid desaturase, Fad3C, partial sequence.
PN   WO200125453-A2.
PD   12-APR-2001.
PA   (UYNE-) UNIV NEWCASTLE VENTURES LTD.
Query Match
Best Local Similarity   29.3%;   Score 71;   Pred. No. 29;   Length 218;

**RESULT 1246**
ID   AAU97208 standard; protein; 228 AA.
DE   Portion of a wheat sugar transport protein encoded by wre1n.pk0006.b4.
PN   US6383776-B1.
PD   07-MAY-2002.
PA   (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match
Best Local Similarity   21.6%;   Score 70.5;   DB 5;   Length 228;

**RESULT 1247**
ID   ABU08333 standard; protein; 228 AA.
DE   Wheat sugar transport protein #3.
PN   US2002178468-A1.
PD   28-NOV-2002.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity   21.6%;   Score 70.5;   DB 6;   Length 228;

**RESULT 1248**
ID   ADG47920 standard; protein; 228 AA.
DE   Wheat Arabidopsis-like sugar transport protein #3.
PN   US2002199217-A1.
PD   26-DEC-2002.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
Query Match
Best Local Similarity   21.6%;   Score 70.5;   DB 8;   Length 228;

**RESULT 1249**
ID   AEE68531 standard; protein; 228 AA.
DE   Triticum aestivum sugar transport protein amino acid sequence SEQ ID 16.
PN   US2005282278-A1.
PD   22-DEC-2005.
PA   (HELE/) HELENIUARIS T G.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
Query Match
Best Local Similarity   21.6%;   Score 70.5;   DB 10;   Length 228;

**RESULT 1250**
Query Match
Best Local Similarity   21.6%;   Score 70.5;   DB 10;   Length 228;

**RESULT 1251**
ID   ABU17430 standard; protein; 275 AA.
DE   Protein encoded by Prokaryotic essential gene #2957.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity   22.8%;   Score 70.5;   DB 6;   Pred. No. 39;   Length 275;

**RESULT 1252**
ID   ADY06253 standard; protein; 283 AA.
DE   Plant full length insert polypeptide seqid 62068.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
Query Match
Best Local Similarity   27.4%;   Score 70.5;   DB 8;   Pred. No. 41;   Length 283;

**RESULT 1253**
ID   ABB55033 standard; protein; 285 AA.
DE   Lactococcus lactis protein malG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity   26.1%;   Score 70.5;   DB 5;   Pred. No. 41;   Length 285;

**RESULT 1254**
ID   ABB05467 standard; protein; 291 AA.
DE   Coriolus versicolor aldo/ketoreductase protein SEQ ID NO:2.
PN   JP2001321171-A.
PD   20-NOV-2001.
PA   (KUBI ) KUBOTA CORP.
PA   (WARI/) WARIISHI H.
Query Match
Best Local Similarity   29.4%;   Score 70.5;   DB 5;   Pred. No. 43;   Length 291;

**RESULT 1255**
ID   ADA35787 standard; protein; 297 AA.
DE   Acinetobacter baumannii protein #2948.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity   24.1%;   Score 70.5;   DB 6;   Pred. No. 44;   Length 297;

**RESULT 1256**
ID   ABM70358 standard; protein; 321 AA.
DE   Photorhabdus luminescens protein sequence #3455.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity   25.9%;   Score 70.5;   DB 6;   Pred. No. 49;   Length 321;

**RESULT 1257**
ID   ABH22355 standard; protein; 330 AA.
DE   Human receptor & membrane associated protein (REMAP) SeqID5.
PN   WO2003104395-A2.
PD   18-DEC-2003.
PA   (INCY-) INCYTE CORP.
Query Match
Best Local Similarity   19.2%;   Score 70.5;   DB 8;   Pred. No. 51;   Length 330;

**RESULT 1258**
ID   ADK68232 standard; protein; 343 AA.
DE   Novel NOVX protein #79.
PN   WO2003085124-A2.
PD   16-OCT-2003.
PA   (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity   24.2%;   Score 70.5;   DB 7;   Pred. No. 53;   Length 343;

ID   ADH72226 standard; protein; 343 AA.
DE   Human protein of the invention NOV55a SEQ ID NO:1122.

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PN  WO0003102155-A2.
PD  11-DEC-2003.
PA  (CURA-) CURAGEN CORP.
    Query Match             30.0%;  Score 70.5;  DB 8;  Length 343;
    Best Local Similarity   30.0%;  Pred. No. 53;
RESULT 1259
ID  ADR49221 standard; protein; 343 AA.
DE  Human NOV10a protein.
PN  US2004162236-A1.
PD  19-AUG-2004.
PA  (ALSO/) ALSOBROOK J.
PA  (BENT/) BENTO P.
PA  (BOLD/) BOLDOG F.
PA  (BURG/) BURGESS C.
PA  (CASM/) CASMAN S.
PA  (BOKO/) BOKOR J C.
PA  (EDIN/) EDINGER S R.
PA  (ELLE/) ELLERMAN K.
PA  (FERN/) FERNANDES E.
PA  (GERL/) GERLACH V.
PA  (GROS/) GROSSE W.
PA  (GUNT/) GUNTHER E.
PA  (GUSE/) GUSEV V.
PA  (HEYE/) HEYES M.
PA  (LEPL/) LEPLEY D.
PA  (LILL/) LI L.
PA  (MACD/) MACDOUGALL J R.
PA  (MALY/) MALYANKAR U M.
PA  (MILL/) MILLET I.
PA  (PATT/) PATTURAJAN M.
PA  (PEYM/) PEYMAN J A.
PA  (RAST/) RASTELLI L.
PA  (RIEG/) RIEGER D.
PA  (SHEN/) SHENOY S.
PA  (SHIM/) SHIMKETS R.
PA  (SMIT/) SMITHSON G.
PA  (STON/) STONE D.
PA  (VERN/) VERNET C.
PA  (VOSS/) VOSS E.
    Query Match             5.9%;  Score 70.5;  DB 8;  Length 343;
    Best Local Similarity   30.0%;  Pred. No. 53;
RESULT 1260
ID  ADY15182 standard; protein; 350 AA.
DE  PRO polypeptide SEQ ID NO 988.
PN  WO2005016962-A2.
PD  24-FEB-2005.
PA  (GETH ) GENENTECH INC.
    Query Match             5.9%;  Score 70.5;  DB 9;  Length 350;
    Best Local Similarity   18.5%;  Pred. No. 55;
RESULT 1261
ID  ADY15180 standard; protein; 350 AA.
DE  PRO polypeptide SEQ ID NO 986.
PN  WO2005016962-A2.
PD  24-FEB-2005.
PA  (GETH ) GENENTECH INC.
    Query Match             5.9%;  Score 70.5;  DB 9;  Length 350;
    Best Local Similarity   18.5%;  Pred. No. 55;
RESULT 1262
ID  ADR40543 standard; protein; 363 AA.
DE  Ovine melatonin receptor O46608 protein.
PN  US2004161823-A1.
PD  19-AUG-2004.
PA  (FEDE/) FEDER J N.
PA  (MINT/) MINTIER G.
PA  (RAMA/) RAMANATHAN C S.
PA  (HAWK/) HAWKEN D R.
    Query Match             5.9%;  Score 70.5;  DB 8;  Length 363;
    Best Local Similarity   23.1%;  Pred. No. 58;
RESULT 1263
ID  AAR69518 standard; protein; 365 AA.
DE  Prostaglandin-EP3-9 receptor.
PN  WO9505052-A1.
PD  05-JAN-1995.
PA  (MERI ) MERCK FROSST CANADA INC.
    Query Match             5.9%;  Score 70.5;  DB 2;  Length 365;
    Best Local Similarity   24.2%;  Pred. No. 58;
RESULT 1264
ID  AAE38521 standard; protein; 365 AA.
DE  Human PTGER3 protein isoform, EP3b.
PN  WO2003064471-A2.
PD  07-AUG-2003.
PA  (DECO-) DECODE GENETICS EHF.
    Query Match             5.9%;  Score 70.5;  DB 7;  Length 365;
    Best Local Similarity   24.2%;  Pred. No. 58;
RESULT 1265
ID  ADI35077 standard; protein; 365 AA.
DE  Human prostaglandin E receptor subtype EP3 (PTGER3) protein #9.
PN  US2003224393-A1.
PD  04-DEC-2003.
PA  (DECO-) DECODE GENETICS EHF.
    Query Match             5.9%;  Score 70.5;  DB 8;  Length 365;
    Best Local Similarity   24.2%;  Pred. No. 58;
RESULT 1266
ID  ADI15889 standard; protein; 365 AA.
DE  Human prostaglandin EP3 receptor #3.
PN  US6670134-B1.
PD  30-DEC-2003.
PA  (ALLE ) ALLERGAN INC.
PA  (UYAR-) UNIV ARIZONA.
    Query Match             5.9%;  Score 70.5;  DB 8;  Length 365;
    Best Local Similarity   24.2%;  Pred. No. 58;
RESULT 1267
ID  ADR67864 standard; protein; 365 AA.
DE  Prostaglandin E2 EP3 III.
PN  WO2004074830-A2.
PD  02-SEP-2004.
PA  (FARB ) BAYER HEALTHCARE AG.
    Query Match             5.9%;  Score 70.5;  DB 8;  Length 365;
    Best Local Similarity   24.2%;  Pred. No. 58;
RESULT 1268
ID  ADS21429 standard; protein; 366 AA.
DE  Bacterial polypeptide #10462.
PN  US2003233675-A1.
PD  18-DEC-2003.
PA  (GOLD/) GOLDMAN B S.
PA  (CHEN/) CHEN X.
PA  (SLAT/) SLATER S C.
PA  (HINK/) HINKLE G J.
PA  (CAOY/) CAO Y.
    Query Match             5.9%;  Score 70.5;  DB 8;  Length 366;
    Best Local Similarity   21.2%;  Pred. No. 59;
RESULT 1269
ID  ADF04358 standard; protein; 367 AA.
DE  Bacterial polypeptide #471.
PN  US6605709-B1.
PD  12-AUG-2003.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match             5.9%;  Score 70.5;  DB 7;  Length 367;
    Best Local Similarity   33.3%;  Pred. No. 59;
RESULT 1270
ID  AAE38520 standard; protein; 374 AA.
DE  Human PTGER3 protein isoform, EP3d.
PN  WO2003064471-A2.
PD  07-AUG-2003.
PA  (DECO-) DECODE GENETICS EHF.
    Query Match             5.9%;  Score 70.5;  DB 7;  Length 374;
    Best Local Similarity   24.2%;  Pred. No. 60;
RESULT 1271
ID  ADI35075 standard; protein; 374 AA.
DE  Human prostaglandin E receptor subtype EP3 (PTGER3) protein #8.
PN  US2003224393-A1.
PD  04-DEC-2003.
PA  (DECO-) DECODE GENETICS EHF.
    Query Match             5.9%;  Score 70.5;  DB 8;  Length 374;
    Best Local Similarity   24.2%;  Pred. No. 60;
RESULT 1272
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ID   AAR48711 standard; protein; 379 AA.
DE   G-protein coupled rat serotonin 2 receptor protein.
PN   WO9405695-A1.
PD   17-MAR-1994.
PA   (UYNY ) UNIV NEW YORK STATE.
     Query Match             22.9%;  Score 70.5;  DB 2;  Length 379;
     Best Local Similarity   22.9%;  Pred. No. 61;
RESULT 1273

ID   AAW02683 standard; peptide; 379 AA.
DE   G-protein coupled rat serotonin 2 receptor.
PN   US5508384-A.
PD   16-APR-1996.
PA   (UYNY ) UNIV NEW YORK STATE.
     Query Match             22.9%;  Score 70.5;  DB 2;  Length 379;
     Best Local Similarity   22.9%;  Pred. No. 61;
RESULT 1274

ID   AAR69517 standard; protein; 388 AA.
DE   Prostaglandin-EP3-21 receptor.
PN   WO9500552-A1.
PD   05-JAN-1995.
PA   (MERI ) MERCK FROSST CANADA INC.
     Query Match             5.9%;   Score 70.5;  DB 2;  Length 388;
     Best Local Similarity   24.2%;  Pred. No. 61;
RESULT 1275

ID   AAE38513 standard; protein; 388 AA.
DE   Human PTGER3 protein isoform, EP3c.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 7;  Length 388;
     Best Local Similarity   24.2%;  Pred. No. 63;
RESULT 1276

ID   ADI35061 standard; protein; 388 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #1.
PN   US20032224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 388;
     Best Local Similarity   24.2%;  Pred. No. 63;
RESULT 1277

ID   ADI15887 standard; protein; 388 AA.
DE   Human prostaglandin EP3 receptor #2.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLR ) ALLERGAN INC.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 388;
     Best Local Similarity   24.2%;  Pred. No. 63;
RESULT 1278

ID   ADI13753 standard; protein; 388 AA.
DE   Human prostaglandin E2 EP3 II polypeptide.
PN   WO2004075813-A2.
PD   10-SEP-2004.
PA   (FARB ) BAYER HEALTHCARE AG.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 388;
     Best Local Similarity   24.2%;  Pred. No. 63;
RESULT 1279

ID   AAR69516 standard; protein; 390 AA.
DE   Prostaglandin-EP3-alpha receptor.
PN   WO9500552-A1.
PD   05-JAN-1995.
PA   (MERI ) MERCK FROSST CANADA INC.
     Query Match             5.9%;   Score 70.5;  DB 2;  Length 390;
     Best Local Similarity   24.2%;  Pred. No. 64;
RESULT 1280

ID   AAE38516 standard; protein; 390 AA.
DE   Human PTGER3 protein isoform, EP3a1.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 7;  Length 390;
     Best Local Similarity   24.2%;  Pred. No. 64;
RESULT 1281

ID   AAE38517 standard; protein; 390 AA.
DE   Human PTGER3 protein isoform, EP3a2.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 7;  Length 390;
     Best Local Similarity   24.2%;  Pred. No. 64;
RESULT 1282

ID   ADI35067 standard; protein; 390 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #4.
PN   US20032224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 390;
     Best Local Similarity   24.2%;  Pred. No. 64;
RESULT 1283

ID   ADI35069 standard; protein; 390 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #5.
PN   US20032224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 390;
     Best Local Similarity   24.2%;  Pred. No. 64;
RESULT 1284

ID   ADI35898 standard; protein; 390 AA.
DE   Human prostaglandin EP3 receptor #4.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLR ) ALLERGAN INC.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 390;
     Best Local Similarity   24.2%;  Pred. No. 64;
RESULT 1285

ID   ADI15885 standard; protein; 390 AA.
DE   Human prostaglandin EP3 receptor #1.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLR ) ALLERGAN INC.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 390;
     Best Local Similarity   24.2%;  Pred. No. 64;
RESULT 1286

ID   ADR70434 standard; protein; 390 AA.
DE   Human prostaglandin E2 EP3 protein.
PN   WO2004074842-A2.
PD   02-SEP-2004.
PA   (FARB ) BAYER HEALTHCARE AG.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 390;
     Best Local Similarity   24.2%;  Pred. No. 64;
RESULT 1287

ID   ADS76168 standard; protein; 390 AA.
DE   Human prostaglandin E2 EP3 I.
PN   WO2004075814-A2.
PD   10-SEP-2004.
PA   (FARB ) BAYER HEALTHCARE AG.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 390;
     Best Local Similarity   24.2%;  Pred. No. 64;
RESULT 1288

ID   AEF06389 standard; protein; 390 AA.
DE   Human PGE receptor type 3a2 SEQ ID NO 7.
PN   WO2005085851-A2.
PD   15-SEP-2005.
PA   (ADRA/) ADRA C N.
     Query Match             5.9%;   Score 70.5;  DB 10;  Length 390;
     Best Local Similarity   24.2%;  Pred. No. 64;
RESULT 1289

ID   AAW57411 standard; protein; 393 AA.
DE   Human prostaglandin EP3-VI receptor.
PN   JP1013185-A.
PD   06-MAY-1998.
PA   (ONOY ) ONO PHARM CO LTD.
     Query Match             5.9%;   Score 70.5;  DB 2;  Length 393;
     Best Local Similarity   24.2%;  Pred. No. 65;
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RESULT 1290
ID   AAE38519 standard; protein; 393 AA.
DE   Human PTGER3 protein isoform, EP3e.
PN   WO200306447l-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 7; Length 393;

RESULT 1291
ID   AAE38523 standard; protein; 393 AA.
DE   Human PTGER3 protein isoform, EP3-VI.
PN   WO200306447l-A2.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 7; Length 393;

RESULT 1292
ID   ADI35081 standard; protein; 393 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11.
PN   US2003224393-Al.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 8; Length 393;

RESULT 1293
ID   ADI35073 standard; protein; 393 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7.
PN   US2003224393-Al.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 8; Length 393;

RESULT 1294
ID   AAW57410 standard; protein; 402 AA.
DE   Human EP3-V receptor.
PN   JP10111318S-A.
PD   06-MAY-1998.
PA   (ONOY ) ONO PHARM CO LTD.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 2; Length 402;

RESULT 1295
ID   ABP81904 standard; protein; 402 AA.
DE   Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 6; Length 402;

RESULT 1296
ID   AAE38522 standard; protein; 402 AA.
DE   Human PTGER3 protein isoform, EP3-V.
PN   WO200306447l-A2.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 7; Length 402;

RESULT 1297
ID   ADI35079 standard; protein; 402 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10.
PN   US2003224393-Al.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 8; Length 402;

RESULT 1298
ID   AD05167 standard; protein; 402 AA.
DE   Protein #69 with increased gene expression in renal cell carcinoma.
PN   WO200403284Z-A2.
PD   22-APR-2004.
PA   (VAND-) VAN ANDEL INST.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 8; Length 402;

RESULT 1299

ID   ADO29620 standard; protein; 402 AA.
DE   Human GPCR PTGER3, SEQ ID NO:722.
PN   WO200404000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 8; Length 402;

RESULT 1300
ID   AD20834 standard; protein; 402 AA.
DE   Human breast cancer marker DKFZp586M0723 protein.
PN   EP1522594-A2.
PD   13-APR-2005.
PA   (FARB ) BAYER HEALTHCARE AG.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 9; Length 402;

RESULT 1301
ID   AAE38514 standard; protein; 407 AA.
DE   Human PTGER3 protein isoform, EP3g.
PN   WO200306447l-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 7; Length 407;

RESULT 1302
ID   ADI35063 standard; protein; 407 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #2.
PN   US2003224393-Al.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 8; Length 407;

RESULT 1303
ID   AAE38518 standard; protein; 425 AA.
DE   Human PTGER3 protein isoform, EP3f.
PN   WO200306447l-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 7; Length 425;

RESULT 1304
ID   ADI35071 standard; protein; 425 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #6.
PN   US2003224393-Al.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 8; Length 425;

RESULT 1305
ID   AEF77677 standard; protein; 425 AA.
DE   Human prostaglandin E receptor 2 (PTGER2) variant 1.
PN   WO200601171-A2.
PD   16-FEB-2006.
PA   (META-) METABOLEX INC.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 10; Length 425;

RESULT 1306
ID   AAE38515 standard; protein; 433 AA.
DE   Human PTGER3 protein isoform, EP3h.
PN   WO200306447l-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 7; Length 433;

RESULT 1307
ID   ADI35065 standard; protein; 433 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3.
PN   US2003224393-Al.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;
     Best Local Similarity   24.2%;
     Score 70.5; DB 8; Length 433;

RESULT 1308
ID   AAW98431 standard; protein; 480 AA.

DE   H. pylori GHPO 446 protein.
PN   WO943478-A1.
PD   08-OCT-1998.
PA   (INNR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA   (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity   23.1%;   Score 70.5;   DB 2;   Length 480;
Query Match   5.9%;   Pred. No. 85;

RESULT 1309
ID   ADY09805 standard; protein; 494 AA.
DE   Plant full length insert polypeptide seqid 65620.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
Best Local Similarity   21.4%;   Score 70.5;   DB 8;   Length 494;
Query Match   5.9%;   Pred. No. 89;

RESULT 1310
ID   ABP40525 standard; protein; 499 AA.
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5370.
PN   US6380370-B1.
PD   30-APR-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity   20.5%;   Score 70.5;   DB 5;   Length 499;
Query Match   5.9%;   Pred. No. 90;

RESULT 1311
ID   ADS06092 standard; protein; 499 AA.
DE   Staphylococcus epidermis polypeptide seqid 5387.
PN   US20040147734-A1.
PD   29-JUL-2004.
PA   (DOUC/) DOUCETTE-STAMM L.
PA   (BUSH/) BUSH D.
Best Local Similarity   20.5%;   Score 70.5;   DB 8;   Length 499;
Query Match   5.9%;   Pred. No. 90;

RESULT 1312
ID   ABU30473 standard; protein; 521 AA.
DE   Protein encoded by Prokaryotic essential gene #16000.
PN   WO2002277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Best Local Similarity   23.7%;   Score 70.5;   DB 6;   Length 521;
Query Match   5.9%;   Pred. No. 95;

RESULT 1313
ID   AAU97213 standard; protein; 539 AA.
DE   Wheat sugar transport protein encoded by w1k8.pk0001.a11.
PN   US6383776-B1.
PD   07-MAY-2002.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
Best Local Similarity   26.0%;   Score 70.5;   DB 5;   Length 539;
Query Match   5.9%;   Pred. No. 1e+02;

RESULT 1314
ID   ABU08338 standard; protein; 539 AA.
DE   Wheat sugar transport protein #4.
PN   US2002178468-A1.
PD   28-NOV-2002.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
Best Local Similarity   26.0%;   Score 70.5;   DB 6;   Length 539;
Query Match   5.9%;   Pred. No. 1e+02;

RESULT 1315
ID   ADG47930 standard; protein; 539 AA.
DE   Wheat Beta-vulgaris-like sugar transport protein #1.
PN   US20021992 17-A1.
PD   26-DEC-2002.
PA   (HELE/) HELENTJARIS T G.
Best Local Similarity   26.0%;   Score 70.5;   DB 5;   Length 539;
Query Match   5.9%;   Pred. No. 1e+02;

RESULT 1316
ID   AEE68541 standard; protein; 539 AA.
DE   Triticum aestivum sugar transport protein amino acid sequence SEQ ID 26.
PN   US2005282278-A1.
PD   22-DEC-2005.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
Best Local Similarity   26.0%;   Score 70.5;   DB 10;   Length 539;
Query Match   5.9%;   Pred. No. 1e+02;

RESULT 1317
ID   ABU27418 standard; protein; 548 AA.
DE   Protein encoded by Prokaryotic essential gene #12945.
PN   WO2002277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Best Local Similarity   24.0%;   Score 70.5;   DB 6;   Length 548;
Query Match   5.9%;   Pred. No. 1e+02;

RESULT 1318
ID   ADN22789 standard; protein; 556 AA.
DE   Bacterial polypeptide #5442.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Best Local Similarity   21.1%;   Score 70.5;   DB 8;   Length 556;
Query Match   5.9%;   Pred. No. 1e+02;

RESULT 1319
ID   ADD46023 standard; protein; 599 AA.
DE   Rat Protein P23978, SEQ ID NO 11695.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO/) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
Best Local Similarity   20.1%;   Score 70.5;   DB 7;   Length 599;
Query Match   5.9%;   Pred. No. 1.2e+02;

RESULT 1320
ID   ABW02687 standard; protein; 599 AA.
DE   Rattus norvegicus neuronal GABA transporter (GAT-1).
PN   US2003143729-A1.
PD   31-JUL-2003.
PA   (SYNA-) SYNAPTIC PHARM CORP.
Best Local Similarity   20.1%;   Score 70.5;   DB 7;   Length 599;
Query Match   5.9%;   Pred. No. 1.2e+02;

RESULT 1321
ID   AAM78767 standard; protein; 600 AA.
DE   Human protein SEQ ID NO 1429.
PN   WO200157190-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
Best Local Similarity   20.1%;   Score 70.5;   DB 4;   Length 600;
Query Match   5.9%;   Pred. No. 1.2e+02;

RESULT 1322
ID   ADJ64315 standard; protein; 662 AA.
DE   Cartilage differentiation inhibiting protein, SEQ ID 10.
PN   WO2004013326-A1.
PD   12-FEB-2004.
PA   (ASAH ) ASAHI KASEI KK.
Best Local Similarity   19.5%;   Score 70.5;   DB 8;   Length 662;
Query Match   5.9%;   Pred. No. 1.3e+02;

RESULT 1323
ID   ABB92892 standard; protein; 700 AA.
DE   Herbicidally active polypeptide SEQ ID NO 2103.
PN   WO200210210-A2.
PD   07-FEB-2002.
PA   (FARB ) BAYER AG.
Best Local Similarity   22.7%;   Score 70.5;   DB 5;   Length 700;
Query Match   5.9%;   Pred. No. 1.4e+02;

RESULT 1324
ID   AAB56721 standard; protein; 717 AA.

DE   Human prostate cancer antigen protein sequence SEQ ID NO:1299.
PN   WO200055174-A1.
PD   21-SEP-2000.
PA   (ROSE/) ROSEN C A.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match 5.9%; Score 70.5; DB 3; Length 717;
     Best Local Similarity 22.4%;
     Pred. No. 1.5e+02;
RESULT 1325
ID   ADG47941 standard; protein; 740 AA.
DE   Arabidopsis thaliana-like sugar transport protein #2.
PN   US200199217-A1.
PN   EP1033405-A2.
PD   26-DEC-2002.
PD   06-SEP-2000.
PA   (HELE/) HELENTJARIS T G.
     Query Match 5.9%; Score 70.5; DB 8; Length 740;
     Best Local Similarity 22.8%;
     Pred. No. 1.6e+02;
RESULT 1326
ID   AAG39555 standard; protein; 766 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 48959.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match 5.9%; Score 70.5; DB 3; Length 766;
     Best Local Similarity 21.3%;
     Pred. No. 1.6e+02;
RESULT 1327
ID   AAG39554 standard; protein; 815 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 48958.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match 5.9%; Score 70.5; DB 3; Length 815;
     Best Local Similarity 21.3%;
     Pred. No. 1.8e+02;
RESULT 1328
ID   AAG39553 standard; protein; 927 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 48957.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match 5.9%; Score 70.5; DB 3; Length 927;
     Best Local Similarity 21.3%;
     Pred. No. 2.1e+02;
RESULT 1329
ID   ABP73754 standard; protein; 1026 AA.
DE   Candida albicans essential protein SEQ ID NO 7591.
PN   WO200253728-A2.
PD   11-JUL-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match 5.9%; Score 70.5; DB 5; Length 1026;
     Best Local Similarity 22.3%;
     Pred. No. 2.4e+02;
RESULT 1330
ID   AAW17057 standard; protein; 1027 AA.
DE   Candida albicans chitin synthase (CHS1).
PN   WO9716540-A1.
PD   09-MAY-1997.
PA   (CHEM-) CHEMGENICS PHARM INC.
     Query Match 5.9%; Score 70.5; DB 2; Length 1027;
     Best Local Similarity 22.3%;
     Pred. No. 2.4e+02;
RESULT 1331
ID   ADH22510 standard; protein; 1147 AA.
DE   Human transporter & ion channel (TRICH) protein SeqIDB.
PN   WO200093444-A2.
PD   13-NOV-2003.
PA   (INCY-) INCYTE CORP.
     Query Match 5.9%; Score 70.5; DB 8; Length 1147;
     Best Local Similarity 19.5%;
     Pred. No. 2.9e+02;
RESULT 1332
ID   ADK18350 standard; protein; 1163 AA.
DE   Human NOVX protein #2.
PN   WO2003057854-A2.
PD   17-JUL-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match 5.9%; Score 70.5; DB 7; Length 1163;
     Best Local Similarity 19.5%;
     Pred. No. 2.9e+02;
RESULT 1333
ID   ADM29274 standard; protein; 1163 AA.
DE   Human novel protein NOV2b.
PN   WO2003064628-A2.
PD   07-AUG-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match 5.9%; Score 70.5; DB 7; Length 1163;
     Best Local Similarity 19.5%;
     Pred. No. 2.9e+02;
RESULT 1334
ID   AAW53863 standard; peptide; 1780 AA.
DE   Human gravin polypeptide.
PN   US5741890-A.
PD   21-APR-1998.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
     Query Match 5.9%; Score 70.5; DB 2; Length 1780;
     Best Local Similarity 34.8%;
     Pred. No. 5.2e+02;
RESULT 1335
ID   AAB15380 standard; protein; 1780 AA.
DE   Human gravin protein sequence.
PN   US6090929-A.
PD   18-JUL-2000.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
     Query Match 5.9%; Score 70.5; DB 3; Length 1780;
     Best Local Similarity 34.8%;
     Pred. No. 5.2e+02;
RESULT 1336
ID   AAO17365 standard; protein; 1781 AA.
DE   Human gravin.
PN   EP1191107-A2.
PD   27-MAR-2002.
PA   (SCHD ) SCHERING AG.
     Query Match 5.9%; Score 70.5; DB 5; Length 1781;
     Best Local Similarity 34.8%;
     Pred. No. 5.2e+02;
RESULT 1337
ID   ABU03477 standard; protein; 1781 AA.
DE   Angiogenesis-associated human protein sequence #22.
PN   WO200279492-A2.
PD   10-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match 5.9%; Score 70.5; DB 6; Length 1781;
     Best Local Similarity 34.8%;
     Pred. No. 5.2e+02;
RESULT 1338
ID   ABB97448 standard; protein; 1783 AA.
DE   Novel human protein SEQ ID NO: 716.
PN   WO200222660-A2.
PD   21-MAR-2002.
PA   (HYSE-) HYSEQ INC.
     Query Match 5.9%; Score 70.5; DB 4; Length 1783;
     Best Local Similarity 34.8%;
     Pred. No. 5.3e+02;
RESULT 1339
ID   ABG21018 standard; protein; 1795 AA.
DE   Novel human diagnostic protein #21009.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match 5.9%; Score 70.5; DB 5; Length 1795;
     Best Local Similarity 34.8%;
     Pred. No. 5.3e+02;
RESULT 1340
ID   AAG34242 standard; protein; 185 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 41631.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match 5.9%; Score 70; DB 3; Length 185;
     Best Local Similarity 26.2%;
     Pred. No. 26;
RESULT 1341
ID   AAG34241 standard; protein; 189 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 41630.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match 5.9%; Score 70; DB 3; Length 189;
     Best Local Similarity 26.2%;
     Pred. No. 27;
RESULT 1342
ID   AAW44944 standard; protein; 225 AA.
DE   Avian infectious bronchitis virus glycoprotein M.
PN   FR2751225-A1.
PD   23-JAN-1998.
PA   (INMR ) RHONE MERIEUX SA.
     Query Match 5.9%; Score 70; DB 2; Length 225;
     Best Local Similarity 21.6%;
     Pred. No. 34;

RESULT 1343
ID   ADB09893 standard; protein; 226 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO:3730.
PN   WO200304830304-A2.
PD   12-JUN-2003.
PA   (AMP ) WYETH HOLDINGS CORP.
     Query Match     5.9%;  Score 70;  DB 6;  Length 226;
     Best Local Similarity   24.1%;  Pred. No. 34;

RESULT 1344
ID   AAG34240 standard; protein; 235 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 41629.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match     5.9%;  Score 70;  DB 3;  Length 235;
     Best Local Similarity   26.2%;  Pred. No. 36;

RESULT 1345
ID   ABB69790 standard; protein; 256 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 36162.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match     5.9%;  Score 70;  DB 4;  Length 256;
     Best Local Similarity   20.2%;  Pred. No. 41;

RESULT 1346
ID   ADS96502 standard; protein; 256 AA.
DE   Drosophila melanogaster protein, SEQ ID NO 123.
PN   WO200403999-A2.
PD   13-MAY-2004.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
     Query Match     5.9%;  Score 70;  DB 8;  Length 256;
     Best Local Similarity   20.2%;  Pred. No. 41;

RESULT 1347
ID   ADT05703 standard; protein; 256 AA.
DE   Haemophilus influenzae (NThi) protein - SEQ ID 739.
PN   WO200478949-A2.
PD   16-SEP-2004.
PA   (CHIL-) CHILDRENS HOSPITAL INC.
     Query Match     5.9%;  Score 70;  DB 8;  Length 256;
     Best Local Similarity   20.2%;  Pred. No. 41;

RESULT 1348
ID   AAG53761 standard; protein; 274 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68478.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match     5.9%;  Score 70;  DB 3;  Length 274;
     Best Local Similarity   18.3%;  Pred. No. 45;

RESULT 1349
ID   AAG53762 standard; protein; 287 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68477.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match     5.9%;  Score 70;  DB 3;  Length 287;
     Best Local Similarity   26.0%;  Pred. No. 48;

RESULT 1350
ID   ABU35677 standard; protein; 292 AA.
DE   Protein encoded by Prokaryotic essential gene #21204.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match     5.9%;  Score 70;  DB 6;  Length 292;
     Best Local Similarity   26.0%;  Pred. No. 49;

RESULT 1351
ID   ADK48488 standard; protein; 307 AA.
DE   Streptococcus pneumoniae protein, Seq ID No 5003.
PN   US5699703-B1.
PD   02-MAR-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match     5.9%;  Score 70;  DB 8;  Length 307;
     Best Local Similarity   22.5%;  Pred. No. 52;

RESULT 1352
ID   AAR72985 standard; protein; 333 AA.
DE   Epsilon opioid receptor.
PN   WO9512670-A1.
PD   11-MAY-1995.
PA   (ALCO-) ALCOHOLISM & DRUG ADDICTION RES FOUND.
     Query Match     5.9%;  Score 70;  DB 2;  Length 333;
     Best Local Similarity   23.6%;  Pred. No. 59;

RESULT 1353
ID   AAY90613 standard; protein; 333 AA.
DE   Human G protein-coupled receptor GPR8.
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
     Query Match     5.9%;  Score 70;  DB 3;  Length 333;
     Best Local Similarity   23.6%;  Pred. No. 59;

RESULT 1354
ID   AAY90647 standard; protein; 333 AA.
DE   Human mutant G protein-coupled receptor GPR8 (T259K).
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
     Query Match     5.9%;  Score 70;  DB 3;  Length 333;
     Best Local Similarity   23.6%;  Pred. No. 59;

RESULT 1355
ID   AAU01297 standard; protein; 333 AA.
DE   Human G-protein receptor 8, GPR 8, mutant N127A.
PN   WO200127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA   (WILL/) WILLIAMS K M.
     Query Match     5.9%;  Score 70;  DB 4;  Length 333;
     Best Local Similarity   23.6%;  Pred. No. 59;

RESULT 1356
ID   AAU01295 standard; protein; 333 AA.
DE   Human G-protein receptor 8, GPR 8.
PN   WO200127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA   (WILL/) WILLIAMS K M.
     Query Match     5.9%;  Score 70;  DB 4;  Length 333;
     Best Local Similarity   23.6%;  Pred. No. 59;

RESULT 1357
ID   AAU01298 standard; protein; 333 AA.
DE   Human G-protein receptor 8, GPR 8, mutant T259E.
PN   WO200127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA   (WILL/) WILLIAMS K M.
     Query Match     5.9%;  Score 70;  DB 4;  Length 333;
     Best Local Similarity   23.6%;  Pred. No. 59;

RESULT 1358
ID   ABB84683 standard; protein; 333 AA.
DE   Human GPR8-ligand related protein #1.
PN   WO200198494-A1.
PD   27-DEC-2001.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match     5.9%;  Score 70;  DB 5;  Length 333;
     Best Local Similarity   23.6%;  Pred. No. 59;

RESULT 1359
ID   ABB84723 standard; protein; 333 AA.
DE   Human GPR8-ligand related protein #3.
PN   WO200198494-A1.
PD   27-DEC-2001.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match     5.9%;  Score 70;  DB 5;  Length 333;
     Best Local Similarity   23.6%;  Pred. No. 59;

RESULT 1360
ID   ABG65918 standard; protein; 333 AA.
DE   G protein-coupled receptor related peptide #6.
PN   WO200243368-A1.
PD   06-JUN-2002.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match     5.9%;  Score 70;  DB 5;  Length 333;
     Best Local Similarity   23.6%;  Pred. No. 59;

RESULT 1361
ID   ABU61448 standard; protein; 333 AA.

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DE   Screening method related protein #1.
PN   WO200293161-Al.
PD   21-NOV-2002.
PA   (TAKE ) TAKEDA CHEM IND LTD.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 6;  Length 333;

RESULT 1362
ID   ABJ37874 standard; protein; 333 AA.
DE   GPR7 ligand related human protein SEQ ID No 84.
PN   WO20021082847-Al.
PD   27-DEC-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 6;  Length 333;

RESULT 1363
ID   ABP81897 standard; protein; 333 AA.
DE   Human GPR8 protein SEQ ID NO:279.
PN   WO2003045994-Al.
PD   05-JUN-2003.
PA   (TAKE ) TAKEDA CHEM IND LTD.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 6;  Length 333;

RESULT 1364
ID   ABR57245 standard; protein; 333 AA.
DE   Human G protein-coupled receptor GPR8 protein SEQ ID NO.84.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 7;  Length 333;

RESULT 1365
ID   ADC22691 standard; protein; 333 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #44.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 7;  Length 333;

RESULT 1366
ID   ADC22535 standard; protein; 333 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #5.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 7;  Length 333;

RESULT 1367
ID   ADC51793 standard; protein; 333 AA.
DE   Human GPR8, SEQ ID 4.
PN   WO20030572236-Al.
PD   17-JUL-2003.
PA   (AREN-) ARENA PHARM INC.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 7;  Length 333;

RESULT 1368
ID   ABR61545 standard; protein; 333 AA.
DE   Human GPR8 receptor polypeptide.
PN   WO2003081234-A2.
PD   02-OCT-2003.
PA   (FARB ) BAYER AG.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 7;  Length 333;

RESULT 1369
ID   ADG41976 standard; protein; 333 AA.
DE   Human GPR8 polypeptide.
PN   JP2003009867-A.
PD   14-JAN-2003.
PA   (TAKE ) TAKEDA CHEM IND LTD.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 7;  Length 333;

RESULT 1370
ID   ADH14008 standard; protein; 333 AA.
DE   Human GPR8.
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PN   US2003105292-Al.
PD   05-JUN-2003.
PA   (CHAL/) CHALMERS D T.
PA   (BEHA/) BEHAN D P.
PA   (LIAW/) LIAW C W.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 7;  Length 333;

RESULT 1371
ID   US2003105292-Al.
DE   Mutated human GPR8.
PN   US2003105292-Al.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 7;  Length 333;

RESULT 1372
ID   ADG12852 standard; protein; 333 AA.
DE   Human GPR8 protein SEQ ID NO:73.
PN   WO2003097795-A2.
PD   27-NOV-2003.
PA   (NORA-) NORAK BIOSCI INC.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 7;  Length 333;

RESULT 1373
ID   ADH14164 standard; protein; 333 AA.
DE   Human wild-type hGPR8 amino acid sequence SEQ ID NO:75.
PN   WO2003097795-A2.
PD   27-NOV-2003.
PA   (NORA-) NORAK BIOSCI INC.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 8;  Length 333;

RESULT 1374
ID   ADO29700 standard; protein; 333 AA.
DE   Human GPCR GPR8, SEQ ID NO:802.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 8;  Length 333;

RESULT 1375
ID   ADO31044 standard; protein; 333 AA.
DE   Human GPR8 protein SEQ ID NO:73.
PN   WO2004041301-Al.
PD   21-MAY-2004.
PA   (TAKE ) TAKEDA CHEM IND LTD.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 8;  Length 333;

RESULT 1376
ID   ADO19919 standard; protein; 333 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.
PN   WO2004049938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 8;  Length 333;

RESULT 1377
ID   ADS14162 standard; protein; 333 AA.
DE   Human GPR8 ligand protein SeqID 73.
PN   WO2004080485-Al.
PD   23-SEP-2004.
PA   (TAKE ) TAKEDA CHEM IND LTD.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 8;  Length 333;

RESULT 1378
ID   ADV24041 standard; protein; 333 AA.
DE   Neuropeptide W antibody associated polypeptide seqid 17.
PN   WO2004106382-Al.
PD   09-DEC-2004.
PA   (TAKE ) TAKEDA PHARM CO LTD.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 59;  DB 9;  Length 333;

RESULT 1379
ID   ADG12854 standard; protein; 347 AA.
DE   Human HA tagged wild-type hGPR8 amino acid sequence SEQ ID NO:77.
PN   WO2003097795-A2.
PD   27-NOV-2003.
PA   (NORA-) NORAK BIOSCI INC.
         Query Match           5.9%;
         Best Local Similarity  23.6%;   Score 70;  Pred. No. 62;  DB 8;  Length 347;

ID   ADH14008 standard; protein; 347 AA.
DE   Human GPR8.
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RESULT 1379
ID   ABG30839 standard; protein; 364 AA.
DE   Human calcium channel protein.
PN   WO20025003-A2.
PA   (FRB ) BAYER AG.
PD   04-JUL-2002.
Query Match             5.9%;
Best Local Similarity  25.0%; Score 70; DB 5; Pred. No. 66; Length 364;

RESULT 1380
ID   ADG12856 standard; protein; 364 AA.
DE   Human hGPR8-enhanced receptor amino acid sequence SEQ ID NO:79.
PN   US2004091946-A1.
PD   13-MAY-2004.
PA   (NORA-) NORAK BIOSCI INC.
PD   27-NOV-2003.
Query Match             5.9%;
Best Local Similarity  23.6%; Score 70; DB 8; Pred. No. 66; Length 364;

RESULT 1381
ID   AD028778 standard; protein; 364 AA.
DE   Human GPR8-enhanced receptor.
PN   WO200512876-A2.
PD   10-FEB-2005.
PA   (NORA-) NORAK BIOSCIENCES INC.
Query Match             5.9%;
Best Local Similarity  23.6%; Score 70; DB 8; Pred. No. 66; Length 364;

RESULT 1382
ID   ADX44597 standard; protein; 364 AA.
DE   Enhanced human G-protein coupled receptor 8 - SEQ ID 56.
PN   WO2005029035-A2.
PD   31-MAR-2005.
PA   (NORA-) NORAK BIOSCIENCES INC.
Query Match             5.9%;
Best Local Similarity  23.6%; Score 70; DB 9; Pred. No. 66; Length 364;

RESULT 1383
ID   ADY83827 standard; protein; 364 AA.
DE   hGPR8-enhanced receptor.
PN   WO2005029035-A2.
PD   31-MAR-2005.
PA   (NORA-) NORAK BIOSCIENCES INC.
Query Match             5.9%;
Best Local Similarity  23.6%; Score 70; DB 9; Pred. No. 66; Length 364;

RESULT 1384
ID   ADG12858 standard; protein; 378 AA.
DE   HA tagged hGPR8-enhanced receptor amino acid sequence SEQ ID NO:81.
PN   WO2003097795-A2.
PD   27-NOV-2003.
PA   (NORA-) NORAK BIOSCI INC.
Query Match             5.9%;
Best Local Similarity  23.6%; Score 70; DB 8; Pred. No. 66; Length 378;

RESULT 1385
ID   ADN49121 standard; protein; 388 AA.
DE   Mouse oxytocin receptor protein.
PN   US2004086881-A1.
PD   06-MAY-2004.
PA   (RAMA/) RAMANATHAN C S.
PA   (GOPA/) GOPAL S.
PA   (MINT/) MINTIER G A.
PA   (FEDE/) FEDER J.
Query Match             5.9%;
Best Local Similarity  24.8%; Score 70; DB 8; Pred. No. 70; Length 388;

RESULT 1386
ID   ADO29591 standard; protein; 388 AA.
DE   Mouse GPCR OXTR, SEQ ID NO:693.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
Query Match             5.9%;
Best Local Similarity  24.8%; Score 70; DB 8; Pred. No. 73; Length 388;

RESULT 1387
ID   ADA54410 standard; protein; 399 AA.
DE   Human protein, SEQ ID 1978.
PN   EP1293569-A2.
PD   19-MAR-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match             5.9%;
Best Local Similarity  22.9%; Score 70; DB 6; Pred. No. 75; Length 399;

RESULT 1388
ID   ABG99947 standard; protein; 399 AA.
DE   Human novel polypeptide #60.
PN   WO20024961-A1.
PD   26-SEP-2002.
PA   (HYSE-) HYSEQ INC.
Query Match             5.9%;
Best Local Similarity  22.9%; Score 70; DB 6; Pred. No. 75; Length 399;

RESULT 1389
ID   ADC96947 standard; protein; 425 AA.
DE   E. faecium protein sequence SEQ ID 6574.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match             5.9%;
Best Local Similarity  25.9%; Score 70; DB 7; Pred. No. 82; Length 425;

RESULT 1390
ID   ADA34110 standard; protein; 470 AA.
DE   Acinetobacter baumannii protein #1271.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match             5.9%;
Best Local Similarity  23.5%; Score 70; DB 6; Pred. No. 96; Length 470;

RESULT 1391
ID   ABM67264 standard; protein; 474 AA.
DE   Photorhabdus luminescens protein sequence #361.
PN   WO2002094867-A2.
PD   28-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
Query Match             5.9%;
Best Local Similarity  22.9%; Score 70; DB 6; Pred. No. 95; Length 474;

RESULT 1392
ID   AAE16787 standard; protein; 475 AA.
DE   Human transporter and ion channel-24 (TRICH-24) protein.
PN   WO200192304-A2.
PD   06-DEC-2001.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match             5.9%;
Best Local Similarity  25.0%; Score 70; DB 5; Pred. No. 96; Length 475;

RESULT 1393
ID   ADA89683 standard; protein; 506 AA.
DE   Staphylococcus aureus antigenic protein #222.
PN   WO2003011899-A2.
PD   13-FEB-2003.
PA   (UYSH-) UNIV SHEFFIELD.
PA   (BIOS-) BIOSYNEXUS INC.
Query Match             5.9%;
Best Local Similarity  20.1%; Score 70; DB 6; Pred. No. 1e+02; Length 506;

RESULT 1394
ID   ABM72414 standard; protein; 506 AA.
DE   Staphylococcus aureus protein #1654.
PN   WO2002094868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
Query Match             5.9%;
Best Local Similarity  20.1%; Score 70; DB 6; Pred. No. 1e+02; Length 506;

RESULT 1395
ID   AAE21176 standard; protein; 540 AA.
DE   Human TRICH-20 protein.
PN   WO200212340-A2.
PD   14-FEB-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match             5.9%;
Best Local Similarity  25.0%; Score 70; DB 5; Pred. No. 1.1e+02; Length 540;

RESULT 1396

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ID   AAM39017 standard; protein; 552 AA.
DE   Human polypeptide SEQ ID NO 2162.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             5.9%;
     Best Local Similarity  25.0%;  Score 70;  DB 4;  Length 552;  Pred. No. 1.2e+02;

RESULT 1397
ID   ABU18262 standard; protein; 602 AA.
DE   Protein encoded by Prokaryotic essential gene #3789.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             5.9%;
     Best Local Similarity  26.4%;  Score 70;  DB 6;  Length 602;  Pred. No. 1.3e+02;

RESULT 1398
ID   ABU33453 standard; protein; 637 AA.
DE   Protein encoded by Prokaryotic essential gene #18980.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             5.9%;
     Best Local Similarity  23.1%;  Score 70;  DB 6;  Length 637;  Pred. No. 1.4e+02;

RESULT 1399
ID   AEB39900 standard; protein; 637 AA.
DE   L. pneumophila protein SEQ ID NO 4232.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP ) INST PASTEUR.
     Query Match             5.9%;
     Best Local Similarity  22.3%;  Score 70;  DB 9;  Length 637;  Pred. No. 1.4e+02;

RESULT 1400
ID   AAY91335 standard; protein; 640 AA.
DE   Group B Streptococcus protein sequence SEQ ID NO:68.
PN   WO200006736-A2.
PD   10-FEB-2000.
PA   (MICR-) MICROBIAL TECHNICS LTD.
     Query Match             5.9%;
     Best Local Similarity  21.4%;  Score 70;  DB 3;  Length 640;  Pred. No. 1.5e+02;

RESULT 1401
ID   AEB36499 standard; protein; 647 AA.
DE   L. pneumophila protein SEQ ID NO 831.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP ) INST PASTEUR.
     Query Match             5.9%;
     Best Local Similarity  22.3%;  Score 70;  DB 9;  Length 647;  Pred. No. 1.5e+02;

RESULT 1402
ID   ABM83818 standard; protein; 695 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:4067.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
     Query Match             5.9%;
     Best Local Similarity  22.3%;  Score 70;  DB 8;  Length 695;  Pred. No. 1.5e+02;

RESULT 1403
ID   ADL04660 standard; protein; 767 AA.
DE   M. catarrhalis protein #426.
PN   US6673910-B1.
PD   06-JAN-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match             5.9%;
     Best Local Similarity  28.6%;  Score 70;  DB 8;  Length 767;  Pred. No. 1.6e+02;

RESULT 1404
ID   AAR53921 standard; protein; 980 AA.
DE   HCV fusion protein corresp. to N-terminal of ORF.
PN   JP06092996-A.
PD   05-APR-1994.
PA   (SHIM/) SHIMOTOYA K.
     Query Match             5.9%;
     Best Local Similarity  21.3%;  Score 70;  DB 8;  Length 980;  Pred. No. 1.9e+02;

RESULT 1405
ID   ADS24062 standard; protein; 1041 AA.
DE   Bacterial polypeptide protein #13095.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match             5.9%;
     Best Local Similarity  24.6%;  Score 70;  DB 2;  Length 1041;  Pred. No. 2.6e+02;

RESULT 1406
ID   ADU69762 standard; protein; 1049 AA.
DE   S agalactiae hyperimmune serum reactive antigen seqid 457.
PN   WO2004092242-A2.
PD   18-NOV-2004.
PA   (INTE-) INTERCELL AG.
     Query Match             5.9%;
     Best Local Similarity  23.4%;  Score 70;  DB 8;  Length 1049;  Pred. No. 2.9e+02;

RESULT 1407
ID   ADU69581 standard; protein; 1049 AA.
DE   S agalactiae hyperimmune serum reactive antigen.seqid 276.
PN   WO2004092242-A2.
PD   18-NOV-2004.
PA   (INTE-) INTERCELL AG.
     Query Match             5.9%;
     Best Local Similarity  18.8%;  Score 70;  DB 8;  Length 1049;  Pred. No. 2.9e+02;

RESULT 1408
ID   ADU69756 standard; protein; 1049 AA.
DE   S agalactiae hyperimmune serum reactive antigen seqid 451.
PN   WO2004092242-A2.
PD   18-NOV-2004.
PA   (INTE-) INTERCELL AG.
     Query Match             5.9%;
     Best Local Similarity  18.8%;  Score 70;  DB 8;  Length 1049;  Pred. No. 2.9e+02;

RESULT 1409
ID   ADV87847 standard; protein; 1049 AA.
DE   Streptococcus agalactiae protein sequence, SEQ ID 241.
PN   FR2824074-A1.
PD   31-OCT-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match             5.9%;
     Best Local Similarity  18.8%;  Score 70;  DB 8;  Length 1049;  Pred. No. 2.9e+02;

RESULT 1410
ID   ADV79100 standard; protein; 1049 AA.
DE   Streptococcus agalactiae protein, SEQ ID 241.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match             5.9%;
     Best Local Similarity  18.8%;  Score 70;  DB 8;  Length 1049;  Pred. No. 2.9e+02;

RESULT 1411
ID   ADV82666 standard; protein; 1049 AA.
DE   Streptococcus agalactiae protein, SEQ ID 3807.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match             5.9%;
     Best Local Similarity  18.8%;  Score 70;  DB 8;  Length 1049;  Pred. No. 2.9e+02;

RESULT 1412
ID   ADV81299 standard; protein; 1049 AA.
DE   Streptococcus agalactiae protein, SEQ ID 2440.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (INSP ) INST PASTEUR.
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PA    (CNRS ) CNRS CENT NAT RECH SCI.
      Query Match    5.9%;   Score 70;    DB 8;   Length 1049;
      Best Local Similarity    18.8%;   Pred. No. 2.9e+02;
RESULT 1413
ID    ADV82607 standard; protein; 1049 AA.
DE    Streptococcus agalactiae protein, SEQ ID 3748.
PN    WO200292818-A2.
PD    21-NOV-2002.
PA    (INSP ) INST PASTEUR.
PA    (CNRS ) CNRS CENT NAT RECH SCI.
      Query Match    5.9%;   Score 70;    DB 8;   Length 1049;
      Best Local Similarity    18.8%;   Pred. No. 2.9e+02;
RESULT 1414
ID    ADP07803 standard; protein; 138 AA.
DE    Human secreted protein, seq id 286.
PN    WO200404200-A2.
PD    21-MAY-2004.
PA    (HUMA-) HUMAN GENOME SCI INC.
      Query Match    5.8%;   Score 70;    DB 8;   Length 138;
      Best Local Similarity    22.0%;   Pred. No. 20;
RESULT 1415
ID    ADA33664 standard; protein; 198 AA.
DE    Acinetobacter baumannii protein #825.
PN    US6562958-B1.
PD    13-MAY-2003.
PA    (GENO-) GENOME THERAPEUTICS CORP.
      Query Match    5.8%;   Score 69.5;   DB 6;   Length 198;
      Best Local Similarity    23.3%;   Pred. No. 33;
RESULT 1416
ID    ADB09276 standard; protein; 201 AA.
DE    Alloiococcus otitis antigenic protein SEQ ID NO:3216.
PN    WO2003048304-A2.
PD    12-JUN-2003.
PA    (AMHP ) WYETH HOLDINGS CORP.
      Query Match    5.8%;   Score 69.5;   DB 6;   Length 201;
      Best Local Similarity    26.0%;   Pred. No. 33;
RESULT 1417
ID    AEB41646 standard; protein; 201 AA.
DE    L. pneumophila protein SEQ ID NO 5978.
PN    WO2005049642-A2.
PD    02-JUN-2005.
PA    (INSP ) INST PASTEUR.
PA    (INRM ) INSERM INST SANTE & RECH MEDICALE.
PA    (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA    (CNRS ) CNRS CENT NAT RECH SCI.
      Query Match    5.8%;   Score 69.5;   DB 9;   Length 201;
      Best Local Similarity    17.6%;   Pred. No. 33;
RESULT 1418
ID    AAU29449 standard; protein; 210 AA.
DE    Human G protein-coupled receptor (GPCR) polypeptide #70.
PN    WO200168858-A2.
PD    20-SEP-2001.
PA    (PHAA ) PHARMACIA & UPJOHN CO.
      Query Match    5.8%;   Score 69.5;   DB 4;   Length 210;
      Best Local Similarity    20.9%;   Pred. No. 35;
RESULT 1419
ID    ABG60737 standard; protein; 210 AA.
DE    Novel G protein coupled receptor (nGPCR-x) #70.
PN    US20020258306-A1.
PD    16-MAY-2002.
PA    (VOGE-/) VOGELI G.
      Query Match    5.8%;   Score 69.5;   DB 4;   Length 210;
      Best Local Similarity    20.9%;   Pred. No. 35;
RESULT 1420
ID    AAU01288 standard; protein; 218 AA.
DE    Brassica napus fatty acid desaturase, Fad3C, mutant partial sequence.
PN    WO200125453-A2.
PD    12-APR-2001.
PA    (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.
      Query Match    5.8%;   Score 69.5;   DB 4;   Length 218;
      Best Local Similarity    29.3%;   Pred. No. 37;
RESULT 1421
ID    ADB09278 standard; protein; 247 AA.
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DE    Alloiococcus otitis antigenic protein SEQ ID NO:3218.
PN    WO2003048304-A2.
PD    12-JUN-2003.
PA    (AMHP ) WYETH HOLDINGS CORP.
      Query Match    5.8%;   Score 69.5;   DB 6;   Length 247;
      Best Local Similarity    26.0%;   Pred. No. 44;
RESULT 1422
ID    ABG66935 standard; protein; 253 AA.
DE    Novel G-protein coupled receptor related protein #12.
PN    WO200240539-A2.
PD    23-MAY-2002.
PA    (CURA-) CURAGEN CORP.
      Query Match    5.8%;   Score 69.5;   DB 5;   Length 253;
      Best Local Similarity    24.2%;   Pred. No. 46;
RESULT 1423
ID    ABB62542 standard; protein; 261 AA.
DE    Drosophila melanogaster polypeptide SEQ ID NO 14418.
PN    WO200171042-A2.
PD    27-SEP-2001.
PA    (PEKE ) PE CORP NY.
      Query Match    5.8%;   Score 69.5;   DB 4;   Length 261;
      Best Local Similarity    27.7%;   Pred. No. 48;
RESULT 1424
ID    ABO80446 standard; protein; 270 AA.
DE    Pseudomonas aeruginosa polypeptide #12621.
PN    US6551795-B1.
PD    22-APR-2003.
PA    (GENO-) GENOME THERAPEUTICS CORP.
      Query Match    5.8%;   Score 69.5;   DB 7;   Length 270;
      Best Local Similarity    22.1%;   Pred. No. 50;
RESULT 1425
ID    ADB86076 standard; protein; 296 AA.
DE    Streptomyces hygroscopicus ABC transporter.
PN    WO2003082909-A1.
PD    09-OCT-2003.
PA    (YEDA ) YEDA RES & DEV CO LTD.
      Query Match    5.8%;   Score 69.5;   DB 4;   Length 296;
      Best Local Similarity    21.0%;   Pred. No. 57;
RESULT 1426
ID    AAG71524 standard; protein; 308 AA.
DE    Human olfactory receptor polypeptide, SEQ ID NO: 1205.
PN    WO200127158-A2.
PD    19-APR-2001.
PA    (DIGI-) DIGISCENTS.
      Query Match    5.8%;   Score 69.5;   DB 4;   Length 308;
      Best Local Similarity    20.9%;   Pred. No. 60;
RESULT 1427
ID    ABB44525 standard; protein; 308 AA.
DE    Human GPCR3 polypeptide SEQ ID NO 9.
PN    WO200174904-A2.
PD    11-OCT-2001.
PA    (CURA-) CURAGEN CORP.
      Query Match    5.8%;   Score 69.5;   DB 4;   Length 308;
      Best Local Similarity    20.9%;   Pred. No. 60;
RESULT 1428
ID    AAU24742 standard; protein; 308 AA.
DE    Human olfactory receptor AOLFR242.
PN    WO200168805-A2.
PD    20-SEP-2001.
PA    (SENO-) SENOMYX INC.
      Query Match    5.8%;   Score 69.5;   DB 4;   Length 308;
      Best Local Similarity    20.9%;   Pred. No. 60;
RESULT 1429
ID    ABP95703 standard; protein; 308 AA.
DE    Human GPCR polypeptide SEQ ID NO 216.
PN    WO200216548-A2.
PD    28-FEB-2002.
PA    (NISC-) JAPAN SCI & TECHNOLOGY CORP.
      Query Match    5.8%;   Score 69.5;   DB 5;   Length 308;
      Best Local Similarity    20.9%;   Pred. No. 60;
RESULT 1430
ID    AAU95729 standard; protein; 308 AA.
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DE   Human olfactory and pheromone G protein-coupled receptor #216.
PN   WO2020224726-A2.
PD   28-MAR-2002.
PA   (CHEM-) CHEMCOM SA.
     Query Match           5.8%;
     Best Local Similarity 20.9%;  Score 69.5;  DB 5;  Length 308;  Pred. No. 60;

RESULT 1431
ID   AAU85362 standard; protein; 308 AA.
DE   G-coupled olfactory receptor #223.
PN   WO20198526-A2.
PD   27-DEC-2001.
PA   (SENO-) SENOMYX INC.
     Query Match           5.8%;
     Best Local Similarity 20.9%;  Score 69.5;  DB 5;  Length 308;  Pred. No. 60;

RESULT 1432
ID   ADC6333 standard; protein; 308 AA.
DE   Human GPCR protein SEQ ID NO.786.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
     Query Match           5.8%;
     Best Local Similarity 20.9%;  Score 69.5;  DB 7;  Length 308;  Pred. No. 60;

RESULT 1433
ID   ABW02126 standard; protein; 308 AA.
DE   Human GPCR3 protein.
PN   US2003195335-A1.
PD   16-OCT-2003.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERES E S.
PA   (CASM/) CASMAN S.
PA   (ALSO/) ALSOBROOK J P.
PA   (BURG/) BURGESS C E.
PA   (PADI/) PADIGARU M.
PA   (TAYL/) TAYLOR S.
PA   (TCHE/) TCHERNEV V T.
PA   (SPYT/) SPYTEK K A.
PA   (LILL/) LI L.
PA   (SHEN/) SHENOY S.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (STON/) STONE D J.
PA   (SMIT/) SMITHSON G.
PA   (MACD/) MACDOUGALL J R.
     Query Match           5.8%;
     Best Local Similarity 20.9%;  Score 69.5;  DB 7;  Length 308;  Pred. No. 60;

RESULT 1434
ID   ABR01671 standard; protein; 316 AA.
DE   Human G protein coupled receptor SEQ ID 202.
PN   WO2003000735-A2.
PD   03-JAN-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match           5.8%;
     Best Local Similarity 20.9%;  Score 69.5;  DB 6;  Length 316;  Pred. No. 63;

RESULT 1435
ID   ADU20551 standard; protein; 317 AA.
DE   A. thaliana At5g67210 homologue.
PN   WO20040092349-A2.
PD   28-OCT-2004.
PA   (BADI ) BASF PLANT SCI GMBH.
     Query Match           5.8%;
     Best Local Similarity 20.9%;  Score 69.5;  DB 6;  Length 317;  Pred. No. 63;

RESULT 1436
ID   ADU20398 standard; protein; 317 AA.
DE   A. thaliana drought tolerance-associated protein At5g67210.
PN   WO20040092349-A2.
PD   28-OCT-2004.
PA   (BADI ) BASF PLANT SCI GMBH.
     Query Match           5.8%;
     Best Local Similarity 33.7%;  Score 69.5;  DB 6;  Length 317;  Pred. No. 63;

RESULT 1437
ID   AAY35360 standard; protein; 321 AA.
DE   Chlamydia pneumoniae involved in the virulence process.
PN   WO927105-A2.
PD   03-JUN-1999.
PA   (GEST ) GENSET.
     Query Match           5.8%;
     Best Local Similarity 21.4%;  Score 69.5;  DB 2;  Length 321;  Pred. No. 64;

RESULT 1438
ID   ADC33485 standard; protein; 321 AA.
DE   Yeast ARV1.
PN   US6566512-B1.
PD   20-MAY-2003.
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
     Query Match           5.8%;
     Best Local Similarity 18.8%;  Score 69.5;  DB 7;  Length 321;  Pred. No. 64;

RESULT 1439
ID   ADE37749 standard; protein; 321 AA.
DE   Yeast ARV1 (ARE-2 Required for viability).
PN   US2003186879-A1.
PD   02-OCT-2003.
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
     Query Match           5.8%;
     Best Local Similarity 18.8%;  Score 69.5;  DB 7;  Length 321;  Pred. No. 64;

RESULT 1440
ID   AAU53139 standard; protein; 327 AA.
DE   Propionibacterium acnes immunogenic protein #14035.
PN   WO20018581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
     Query Match           5.8%;
     Best Local Similarity 25.5%;  Score 69.5;  DB 4;  Length 327;  Pred. No. 66;

RESULT 1441
ID   ABM49658 standard; protein; 327 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #14334.
PN   WO2003033515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
     Query Match           5.8%;
     Best Local Similarity 25.5%;  Score 69.5;  DB 6;  Length 327;  Pred. No. 66;

RESULT 1442
ID   ADH10684 standard; protein; 354 AA.
DE   Rat Sprague-Dawley putative GCR polypeptide.
PN   WO2003104484-A1.
PD   18-DEC-2003.
PA   (META-) METABOLEX INC.
     Query Match           5.8%;
     Best Local Similarity 22.0%;  Score 69.5;  DB 8;  Length 354;  Pred. No. 73;

RESULT 1443
ID   AAY05489 standard; protein; 382 AA.
DE   Human EDG-2 protein sequence.
PN   WO919513-A2.
PD   22-APR-1999.
PA   (LXRB-) LXR BIOTECHNOLOGY INC.
     Query Match           5.8%;
     Best Local Similarity 20.2%;  Score 69.5;  DB 2;  Length 382;  Pred. No. 81;

RESULT 1444
ID   AAU00302 standard; protein; 382 AA.
DE   LPA receptor-related amino acid sequence #1.
PN   WO20011838-A2.
PD   22-FEB-2001.
PA   (ATAI-) ATAIRGIN TECHNOLOGIES INC.
     Query Match           5.8%;
     Best Local Similarity 20.2%;  Score 69.5;  DB 4;  Length 382;  Pred. No. 81;

RESULT 1445
ID   ABG76099 standard; protein; 382 AA.
DE   Human lysophosphatidic acid (lPA) receptor EDG-1.
PN   US6485922-B1.
PD   26-NOV-2002.
PA   (ATAI-) ATAIRGIN TECHNOLOGIES INC.
     Query Match           5.8%;
     Best Local Similarity 20.2%;  Score 69.5;  DB 6;  Length 382;  Pred. No. 81;

RESULT 1446
ID   ABB47613 standard; protein; 400 AA.
DE   Listeria monocytogenes protein #317.
PN   WO20017335-A2.
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PD  18-OCT-2001.
PA  (INSP ) INST PASTEUR.
    Query Match
    Best Local Similarity     22.9%;    Score 69.5;  DB 5;  Length 400;
RESULT 1447
ID  ABU32698 standard; protein; 400 AA.
DE  Protein encoded by Prokaryotic essential gene #18225.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
    Query Match
    Best Local Similarity     22.9%;    Score 69.5;  DB 6;  Length 400;
RESULT 1448
ID  ADL12060 standard; protein; 401 AA.
DE  Drosophila dmTrp1 protein.
PN  WO200302137-A2.
PD  09-JAN-2003.
PA  (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
    Query Match
    Best Local Similarity     20.9%;    Score 69.5;  DB 7;  Length 401;
RESULT 1449
ID  ABB60948 standard; protein; 415 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 9636.
PN  WO200171042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
    Query Match
    Best Local Similarity     20.9%;    Score 69.5;  DB 4;  Length 415;
RESULT 1450
ID  ADL12059 standard; protein; 415 AA.
DE  Drosophila dmTrp1alt2 protein.
PN  WO200302137-A2.
PD  09-JAN-2003.
PA  (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
    Query Match
    Best Local Similarity     20.9%;    Score 69.5;  DB 7;  Length 415;
RESULT 1451
ID  ABB66992 standard; protein; 428 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 27768.
PN  WO200171042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
    Query Match
    Best Local Similarity     20.9%;    Score 69.5;  DB 4;  Length 428;
RESULT 1452
ID  ADL12058 standard; protein; 428 AA.
DE  Drosophila dmTrp1alt1 protein.
PN  WO200302137-A2.
PD  09-JAN-2003.
PA  (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
    Query Match
    Best Local Similarity     20.9%;    Score 69.5;  DB 7;  Length 428;
RESULT 1453
ID  AAY41284 standard; protein; 444 AA.
DE  Arabidopsis thaliana protein fragment 453 AA.
PN  EP103405-A2.
PD  06-SEP-2000.
PA  (UYVA-) UNIV VANDERBILT.
    Query Match
    Best Local Similarity     20.9%;    Score 69.5;  DB 2;  Length 444;
RESULT 1454
ID  AAG30875 standard; protein; 453 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 36988.
PN  EP103405-A2.
PD  06-SEP-2000.
PA  (UYVA-) UNIV VANDERBILT.
    Query Match
    Best Local Similarity     23.6%;    Score 69.5;  DB 2;  Length 453;
RESULT 1455
ID  ADK47327 standard; protein; 453 AA.
DE  Streptococcus pneumoniae protein, Seq ID No 3842.
PN  US669703-B1.
PD  02-MAR-2004.
PA  (GENO-) GENOME THERAPEUTICS CORP.

    Query Match
    Best Local Similarity     24.4%;    Score 69.5;  DB 8;  Length 453;
RESULT 1456
ID  ADR95087 standard; protein; 461 AA.
DE  Novel S. pneumoniae protein sequence, SEQ ID 3722.
PN  US680744-B1.
PD  05-OCT-2004.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match
    Best Local Similarity     24.4%;    Score 69.5;  DB 9;  Length 461;
RESULT 1457
ID  AEA58957 standard; protein; 461 AA.
DE  Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:3722.
PN  US200513640441-A1.
PD  23-JUN-2005.
PA  (DOUC/) DOUCETTE-STAMM L A.
PA  (BUSH/) BUSH D.
    Query Match
    Best Local Similarity     24.4%;    Score 69.5;  DB 8;  Length 461;
RESULT 1458
ID  AAG30874 standard; protein; 476 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 36987.
PN  EP103405-A2.
PD  06-SEP-2000.
PA  (UYVA-) UNIV VANDERBILT.
    Query Match
    Best Local Similarity     23.3%;    Score 69.5;  DB 3;  Length 476;
RESULT 1459
ID  ADN22349 standard; protein; 477 AA.
DE  Bacterial polypeptide #5002.
PN  US200323675-A1.
PD  18-DEC-2003.
PA  (CAOY/) CAO Y.
PA  (HINK/) HINKLE G J.
PA  (SLAT/) SLATER S C.
PA  (CHEN/) CHEN X.
PA  (GOLD/) GOLDMAN B S.
    Query Match
    Best Local Similarity     21.2%;    Score 69.5;  DB 8;  Length 477;
RESULT 1460
ID  ADS28512 standard; protein; 490 AA.
DE  Bacterial polypeptide #17545.
PN  US200323675-A1.
PD  18-DEC-2003.
PA  (CAOY/) CAO Y.
PA  (HINK/) HINKLE G J.
PA  (SLAT/) SLATER S C.
PA  (CHEN/) CHEN X.
PA  (GOLD/) GOLDMAN B S.
    Query Match
    Best Local Similarity     23.5%;    Score 69.5;  DB 8;  Length 490;
RESULT 1461
ID  ABO61637 standard; protein; 494 AA.
DE  Klebsiella pneumoniae polypeptide seqid 8154.
PN  US661036-B1.
PD  26-AUG-2003.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match
    Best Local Similarity     22.0%;    Score 69.5;  DB 7;  Length 494;
RESULT 1462
ID  AAY41278 standard; protein; 500 AA.
DE  Fusion protein containing rabbit prostaglandin E2EP3 receptor.
PN  WO995303-A1.
PD  21-OCT-1999.
PA  (UYVA-) UNIV VANDERBILT.
    Query Match
    Best Local Similarity     23.6%;    Score 69.5;  DB 2;  Length 500;
RESULT 1463
ID  AAG30873 standard; protein; 503 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 36986.
PN  EP103405-A2.
PD  06-SEP-2000.
PA  (UYVA-) UNIV VANDERBILT.
    Query Match
    Best Local Similarity     23.3%;    Score 69.5;  DB 3;  Length 503;

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RESULT 1464
ID   AAY92829 standard; protein; 535 AA.
DE   C. pneumoniae CPN100557 processed antigen.
PN   WO200024765-A2.
PD   04-MAY-2000.
PA   (CONN-) CONNAUGHT LAB LTD.
     Query Match
     Best Local Similarity   21.4%;   Score 69.5;   DB 3;   Length 535;

RESULT 1465
ID   ADR13717 standard; protein; 540 AA.
DE   Amidase, SEQ ID 54.
PN   WO200406 9848-A2.
PD   19-AUG-2004.
PA   (DIVE-) DIVERSA CORP.
     Query Match
     Best Local Similarity   23.7%;   Score 69.5;   DB 8;   Length 540;

RESULT 1466
ID   AAY92828 standard; protein; 547 AA.
DE   C. pneumoniae CPN100557 antigen.
PN   WO200024765-A2.
PD   04-MAY-2000.
PA   (CONN-) CONNAUGHT LAB LTD.
     Query Match
     Best Local Similarity   21.4%;   Score 69.5;   DB 3;   Length 547;

RESULT 1467
ID   ABU26764 standard; protein; 547 AA.
DE   Protein encoded by Prokaryotic essential gene #12291.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match
     Best Local Similarity   21.4%;   Score 69.5;   DB 6;   Length 547;

RESULT 1468
ID   ABU31940 standard; protein; 551 AA.
DE   Protein encoded by Prokaryotic essential gene #17467.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match
     Best Local Similarity   23.6%;   Score 69.5;   DB 6;   Length 551;

RESULT 1469
ID   AAY01650 standard; protein; 557 AA.
DE   A protein with cation transporting activity.
PN   WO9913072-A1.
PD   18-MAR-1999.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
     Query Match
     Best Local Similarity   26.3%;   Score 69.5;   DB 2;   Length 557;

RESULT 1470
ID   AAY83929 standard; protein; 557 AA.
DE   Human carnitine transporter protein OCTN2.
PN   WO200014210-A1.
PD   16-MAR-2000.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
     Query Match
     Best Local Similarity   26.3%;   Score 69.5;   DB 3;   Length 557;

RESULT 1471
ID   ABG03029 standard; protein; 557 AA.
DE   Novel human diagnostic protein #3020.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match
     Best Local Similarity   26.3%;   Score 69.5;   DB 4;   Length 557;

RESULT 1472
ID   ABB82979 standard; protein; 557 AA.
DE   Human SLC22A related protein-GenBank Identifier No. GI# 3242598.
PN   WO200299053-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
     Query Match
     Best Local Similarity   26.3%;   Score 69.5;   DB 6;   Length 557;

RESULT 1473
ID   ABB82980 standard; protein; 557 AA.
DE   Human SLC22A related protein-GenBank Identifier No. GI# 4507005.
PN   WO200299053-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
     Query Match
     Best Local Similarity   26.3%;   Score 69.5;   DB 6;   Length 557;

RESULT 1474
ID   ABO07242 standard; protein; 557 AA.
DE   Human p53 modifying protein, SEQ ID 202.
PN   WO200299122-A1.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
     Query Match
     Best Local Similarity   26.3%;   Score 69.5;   DB 7;   Length 557;

RESULT 1475
ID   ADE09321 standard; protein; 557 AA.
DE   Novel protein-related contig polypeptide sequence #387.
PN   WO200305 4152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match
     Best Local Similarity   26.3%;   Score 69.5;   DB 7;   Length 557;

RESULT 1476
ID   ADE09261 standard; protein; 557 AA.
DE   Novel protein-related contig polypeptide sequence #327.
PN   WO200305 4152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match
     Best Local Similarity   26.3%;   Score 69.5;   DB 7;   Length 557;

RESULT 1477
ID   ADP23817 standard; protein; 557 AA.
DE   PRO polypeptide SEQ ID NO:995.
PN   WO200404 1170-A2.
PD   21-MAY-2004.
PA   (GETH-) GENENTECH INC.
     Query Match
     Best Local Similarity   26.3%;   Score 69.5;   DB 8;   Length 557;

RESULT 1478
ID   ADY79867 standard; protein; 557 AA.
DE   Amino acid sequence of a human SLC22A5 polypeptide.
PN   WO200506 2724-A2.
PD   24-MAR-2005.
PA   (FARB-) BAYER HEALTHCARE AG.
     Query Match
     Best Local Similarity   26.3%;   Score 69.5;   DB 9;   Length 557;

RESULT 1479
ID   ADA34637 standard; protein; 559 AA.
DE   Acinetobacter baumannii protein #1798.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match
     Best Local Similarity   20.2%;   Score 69.5;   DB 7;   Length 559;

RESULT 1480
ID   ABG02908 standard; protein; 564 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9425.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match
     Best Local Similarity   23.6%;   Score 69.5;   DB 7;   Length 564;

RESULT 1481
ID   ABB89665 standard; protein; 568 AA.
DE   Human polypeptide SEQ ID NO 2041.
PN   WO200190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match
     Best Local Similarity   22.4%;   Score 69.5;   DB 5;   Length 568;

RESULT 1482
ID   ADB65515 standard; protein; 573 AA.
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DE   Human protein encoded by clone TESTI20271790.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match             5.8%;  Score 69.5;  DB 7;  Length 573;
  Best Local Similarity 22.7%;  Pred. No. 1.4e+02;

RESULT 1483
ID   ABB47410 standard; protein; 579 AA.
DE   Listeria monocytogenes protein #114.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP ) INST PASTEUR.
Query Match             5.8%;  Score 69.5;  DB 5;  Length 579;
  Best Local Similarity 21.1%;  Pred. No. 1.4e+02;

RESULT 1484
ID   ABU32703 standard; protein; 579 AA.
DE   Protein encoded by Prokaryotic essential gene #18230.
PN   WO200271183-A2.
PD   13-JUN-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match             5.8%;  Score 69.5;  DB 6;  Length 579;
  Best Local Similarity 21.1%;  Pred. No. 1.4e+02;

RESULT 1485
ID   ABP65234 standard; protein; 599 AA.
DE   Hypoxia-regulated protein #108.
PN   WO200246465-A2.
PD   03-OCT-2002.
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match             5.8%;  Score 69.5;  DB 5;  Length 599;
  Best Local Similarity 19.6%;  Pred. No. 1.5e+02;

RESULT 1486
ID   AAE38584 standard; protein; 599 AA.
DE   Human GAT1 GABA transporter protein.
PN   WO200306157 3-A2.
PD   31-JUL-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match             5.8%;  Score 69.5;  DB 7;  Length 599;
  Best Local Similarity 19.6%;  Pred. No. 1.5e+02;

RESULT 1487
ID   ADD46025 standard; protein; 599 AA.
DE   Human Protein P30531, SEQ ID NO 11697.
PN   WO200301647 5-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
Query Match             5.8%;  Score 69.5;  DB 7;  Length 599;
  Best Local Similarity 19.6%;  Pred. No. 1.5e+02;

RESULT 1488
ID   AAY41285 standard; protein; 656 AA.
DE   CI-77A-TL fusion protein encoded by plasmid pLJM5-42T.
PN   WO9953033-A1.
PD   21-OCT-1999.
PA   (UVA-) UNIV VANDERBILT.
Query Match             5.8%;  Score 69.5;  DB 2;  Length 656;
  Best Local Similarity 19.6%;  Pred. No. 1.7e+02;

RESULT 1489
ID   ABP40194 standard; protein; 660 AA.
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5039.
PN   US6380370-B1.
PD   30-APR-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match             5.8%;  Score 69.5;  DB 5;  Length 660;
  Best Local Similarity 23.6%;  Pred. No. 1.7e+02;

RESULT 1490
ID   ADS07250 standard; protein; 660 AA.
DE   Staphylococcus epidermis polypeptide seqid 6545.
PN   US200414773 4-A1.
PD   29-JUL-2004.
PA   (DOUC/) DOUCETTE-STAMM L.
PA   (BUSH/) BUSH D.
Query Match             5.8%;  Score 69.5;  DB 5;  Length 660;
  Best Local Similarity 27.2%;  Pred. No. 1.7e+02;
Query Match             5.8%;  Score 69.5;  DB 8;  Length 660;
  Best Local Similarity 27.2%;  Pred. No. 1.7e+02;

RESULT 1491
ID   AAY17390 standard; protein; 663 AA.
DE   Human vesicle membrane protein-like protein 3.
PN   WO9921994-A2.
PD   06-MAY-1999.
PA   (INCY-) INCYTE PHARM INC.
Query Match             5.8%;  Score 69.5;  DB 2;  Length 663;
  Best Local Similarity 22.0%;  Pred. No. 1.7e+02;

RESULT 1492
ID   ADM83092 standard; protein; 663 AA.
DE   Human vesicle membrane protein (VMP)2.
PN   US2003175787-A1.
PD   18-SEP-2003.
PA   (INCY-) INCYTE CORP.
Query Match             5.8%;  Score 69.5;  DB 7;  Length 663;
  Best Local Similarity 22.0%;  Pred. No. 1.7e+02;

RESULT 1493
ID   ADJ64317 standard; protein; 663 AA.
DE   Cartilage differentiation inhibiting protein, SEQ ID 12.
PN   WO200401332 6-A1.
PD   12-FEB-2004.
PA   (ASAH ) ASAHI KASEI KK.
Query Match             5.8%;  Score 69.5;  DB 8;  Length 663;
  Best Local Similarity 22.0%;  Pred. No. 1.7e+02;

RESULT 1494
ID   ADQ96536 standard; protein; 663 AA.
DE   T cell activation associated protein #357.
PN   WO200405880 5-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match             5.8%;  Score 69.5;  DB 8;  Length 663;
  Best Local Similarity 22.0%;  Pred. No. 1.7e+02;

RESULT 1495
ID   ADY19824 standard; protein; 663 AA.
DE   PRO polypeptide SEQ ID NO 5630.
PN   WO200501696 2-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
Query Match             5.8%;  Score 69.5;  DB 9;  Length 663;
  Best Local Similarity 22.0%;  Pred. No. 1.7e+02;

RESULT 1496
ID   ADY14394 standard; protein; 663 AA.
DE   PRO polypeptide SEQ ID NO 200.
PN   WO200501696 2-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
Query Match             5.8%;  Score 69.5;  DB 9;  Length 663;
  Best Local Similarity 22.0%;  Pred. No. 1.7e+02;

RESULT 1497
ID   ADO09827 standard; protein; 681 AA.
DE   Hamster SGLT homologue protein SEQ ID NO:50.
PN   WO200403940 5-A1.
PD   13-MAY-2004.
PA   (TAKE ) TAKEDA CHEM IND LTD.
Query Match             5.8%;  Score 69.5;  DB 8;  Length 681;
  Best Local Similarity 24.5%;  Pred. No. 1.8e+02;

RESULT 1498
ID   ABU41908 standard; protein; 695 AA.
DE   Protein encoded by Prokaryotic essential gene #27435.
PN   WO200271183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match             5.8%;  Score 69.5;  DB 6;  Length 695;
  Best Local Similarity 24.3%;  Pred. No. 1.9e+02;

RESULT 1499
ID   AD748367 standard; protein; 764 AA.
DE   Maize oil-associated gene protein #26.
PN   US200402520 2-A1.
PD   05-FEB-2004.
PA   (LAUR/) LAURIE C. C.
PA   (RAVA/) RAVANELLO M.
PA   (SAVA/) SAVAGE T.
PA   (LEDE/) LEDEAUX J R.
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PA    (ROGE/) ROGERS J A.
      Query Match        5.8%;    Score 69.5;   DB 8;   Length 764;
      Best Local Similarity   21.0%;   Pred. No. 2.1e+02;
RESULT 1500
ID    ABU43821 standard; protein; 801 AA.
DE    Protein encoded by Prokaryotic essential gene #29348.
PN    WO2002771183-A2.
PD    03-OCT-2002.
PA    (ELIT-) ELITRA PHARM INC.
      Query Match        5.8%;    Score 69.5;   DB 6;   Length 801;
      Best Local Similarity   19.9%;   Pred. No. 2.3e+02;

OM protein - protein search, using sw model

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GenCore version 5.1.9

Run on: October 31, 2006, 02:22:19 ; Search time 52 Seconds
(without alignments)
393.888 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
Sequence: 1 MNHLPEDMENALTGSOSSHA..........EAGSEEAEEKQDSEKPLLEL 234

Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
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4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 669.5 | 56.0 | 176 | 2 | US-10-104-047-2567 | Sequence 2567, Ap |
| 2 | 664 | 55.6 | 445 | 1 | US-08-691-814B-6 | Sequence 6, Appli |
| 3 | 85.5 | 7.2 | 449 | 2 | US-09-949-016-8594 | Sequence 8594, Ap |
| 4 | 82.5 | 6.9 | 341 | 1 | US-08-846-762-92 | Sequence 92, Appl |
| 5 | 80.5 | 6.7 | 350 | 2 | US-10-489-039A-9711 | Sequence 9711, Ap |
| 6 | 80.5 | 6.7 | 891 | 2 | US-10-226-629A-16 | Sequence 16, Appl |
| 7 | 79.5 | 6.7 | 406 | 2 | US-09-171-699-4 | Sequence 4, Appl |
| 8 | 79.5 | 6.7 | 406 | 5 | PCT-US94-02107-2 | Sequence 2, Appli |
| 9 | 79.5 | 6.7 | 723 | 2 | US-09-976-594-503 | Sequence 503, App |
| 10 | 78.5 | 6.6 | 723 | 2 | US-09-270-767-41033 | Sequence 41033, A |
| 11 | 78.5 | 6.6 | 221 | 2 | US-09-270-767-56249 | Sequence 56249, A |
| 12 | 78.5 | 6.6 | 766 | 2 | US-09-724-653-2 | Sequence 2, Appli |
| 13 | 78.5 | 6.6 | 766 | 2 | US-09-724-653-14 | Sequence 14, Appl |
| 14 | 78.5 | 6.6 | 766 | 2 | US-09-724-653-15 | Sequence 15, Appl |
| 15 | 78 | 6.5 | 228 | 2 | US-09-833-752-9 | Sequence 9, Appli |
| 16 | 78 | 6.5 | 251 | 2 | US-09-270-767-43373 | Sequence 43373, A |
| 17 | 78 | 6.5 | 355 | 2 | US-09-938-719-9 | Sequence 9, Appli |
| 18 | 78 | 6.5 | 355 | 2 | US-09-938-703B-9 | Sequence 9, Appli |
| 19 | 78 | 6.5 | 355 | 2 | US-09-939-226B-9 | Sequence 9, Appli |
| 20 | 78 | 6.5 | 355 | 2 | US-10-226-629A-15 | Sequence 15, Appli |
| 21 | 77.5 | 6.5 | 892 | 1 | US-10-226-629A-15 | Sequence 15, Appl |
| 22 | 77 | 6.5 | 355 | 2 | US-08-466-103A-14 | Sequence 14, Appl |
| 23 | 77 | 6.4 | 353 | 2 | US-08-466-103A-14 | Sequence 14, Appl |
| 24 | 77 | 6.4 | 353 | 2 | US-09-479-195-2 | Sequence 2, Appli |
| 25 | 76.5 | 6.4 | 435 | 2 | US-09-489-039A-12344 | Sequence 12344, A |
| 26 | 76.5 | 6.4 | 494 | 1 | US-08-464-340A-4 | Sequence 4, Appli |
| 27 | 76.5 | 6.4 | 494 | 5 | PCT-US94-08449A-4 | Sequence 4, Appli |
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| 518 | 66.5 | 5.6 | 2955 | 1 | US-09-249-843-3 | Sequence 3, Appli |
| 519 | 66.5 | 5.6 | 2955 | 2 | US-08-444-818-138 | Sequence 138, App |
| 520 | 66.5 | 5.6 | 2894 | 2 | US-08-444-818-138 | Sequence 138, App |
| 521 | 66.5 | 5.6 | 3010 | 2 | US-08-440-103-36 | Sequence 36, Appl |
| 522 | 66.5 | 5.6 | 3011 | 2 | US-08-440-542-36 | Sequence 36, Appl |
| 523 | 66.5 | 5.6 | 3011 | 2 | US-07-910-760-10 | Sequence 10, Appl |
| 524 | 66.5 | 5.6 | 3011 | 1 | US-08-509-519-10 | Sequence 10, Appl |
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| 527 | 66.5 | 5.6 | 3011 | 1 | US-08-440-210-36 | Sequence 36, Appl |
| 528 | 66.5 | 5.6 | 3011 | 2 | US-08-444-818-177 | Sequence 177, App |
| 529 | 66.5 | 5.6 | 3011 | 2 | US-09-529-169A-6 | Sequence 6, Appli |
| 530 | 66.5 | 5.6 | 3011 | 2 | US-09-014-416-5 | Sequence 5, Appli |
| 531 | 66.5 | 5.6 | 3011 | 2 | US-09-388-874-2 | Sequence 2, Appli |
| 532 | 66.5 | 5.6 | 3011 | 2 | US-09-046-604-36 | Sequence 36, Appl |
| 533 | 66.5 | 5.6 | 3011 | 2 | US-08-442-805A-3 | Sequence 3, Appli |
| 534 | 66.5 | 5.6 | 3011 | 2 | US-09-529-169A-6 | Sequence 6, Appli |
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| 536 | 66.5 | 5.6 | 3011 | 6 | US-08-483-799-6 | Sequence 6, Appli |
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| 539 | 66.5 | 5.6 | 3011 | 5 | PCT-US91-02225-10 | Sequence 10, Appl |
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| 542 | 66 | 5.5 | 248 | 2 | US-09-258-634-4 | Sequence 4, Appli |
| 543 | 66 | 5.5 | 282 | 2 | US-09-107-532A-5717 | Sequence 5717, Ap |
| 544 | 66 | 5.5 | 289 | 2 | US-09-134-001C-2917 | Sequence 2917, Ap |
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| 546 | 66 | 5.5 | 316 | 2 | US-09-328-352-6692 | Sequence 6692, Ap |
| 547 | 66 | 5.5 | 318 | 2 | US-09-270-767-45996 | Sequence 45996, A |
| 548 | 66 | 5.5 | 370 | 2 | US-09-172-353-7 | Sequence 7, Appli |
| 549 | 66 | 5.5 | 370 | 2 | US-08-776-971-140 | Sequence 140, Appl |
| 550 | 66 | 5.5 | 370 | 2 | US-09-799-955-7 | Sequence 7, Appli |
| 551 | 66 | 5.5 | 370 | 2 | US-09-576-290-140 | Sequence 140, App |
| 552 | 66 | 5.5 | 381 | 1 | US-08-845-566-3 | Sequence 3, Appli |
| 553 | 66 | 5.5 | 381 | 1 | US-09-716-147-140 | Sequence 140, Appl |
| 554 | 66 | 5.5 | 381 | 1 | US-08-467-948A-28 | Sequence 28, Appl |
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| 556 | 66 | 5.5 | 381 | 2 | US-08-467-947A-28 | Sequence 28, Appl |
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| 558 | 66 | 5.5 | 381 | 2 | US-09-518-383-18 | Sequence 18, Appl |
| 559 | 66 | 5.5 | 390 | 3 | PCT-US96-10618-4 | Sequence 4, Appl |
| 560 | 66 | 5.5 | 390 | 2 | US-09-944-049-20 | Sequence 20, Appl |
| 561 | 66 | 5.5 | 405 | 2 | US-09-944-049-22 | Sequence 22, Appl |
| 562 | 66 | 5.5 | 412 | 3 | US-10-138-701-59 | Sequence 59, Appl |
| 563 | 66 | 5.5 | 412 | 3 | US-09-944-049-22 | Sequence 22, Appli |
| 564 | 66 | 5.5 | 433 | 3 | US-09-134-000C-6536 | Sequence 6536, Ap |
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| 566 | 66 | 5.5 | 447 | 3 | US-10-077-870-2 | Sequence 2, Appli |
| 567 | 66 | 5.5 | 450 | 3 | US-09-825-923-4 | Sequence 4, Appli |
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| 569 | 66 | 5.5 | 582 | 2 | US-09-721-870-179 | Sequence 179, App |
| 570 | 66 | 5.5 | 583 | 2 | US-09-270-767-38131 | Sequence 38131, A |
| 571 | 66 | 5.5 | 583 | 2 | US-09-767-53348 | Sequence 53348, A |
| 572 | 66 | 5.5 | 1250 | 2 | US-09-938-291A-9 | Sequence 9, Appl |
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| 575 | 65.5 | 5.5 | 155 | 2 | US-09-134-000C-3721 | Sequence 3721, Ap |
| 576 | 65.5 | 5.5 | 166 | 2 | US-09-134-001C-4279 | Sequence 4279, Ap |
| 577 | 65.5 | 5.5 | 210 | 2 | US-09-487-558B-320 | Sequence 320, App |
| 578 | 65.5 | 5.5 | 210 | 2 | US-09-538-092-121 | Sequence 121, App |
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| 586 | 65.5 | 5.5 | 459 | 2 | US-08-694-519-4 | Sequence 4, Appli |
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| 607 | 65.5 | 5.5 | 1417 | 2 | US-09-753-385-4 | Sequence 4, Appli |
| 608 | 65.5 | 5.4 | 1427 | 2 | US-09-487-558B-354 | Sequence 354, App |
| 609 | 65 | 5.4 | 126 | 2 | US-09-107-532A-3813 | Sequence 3813, Ap |
| 610 | 65 | 5.4 | 176 | 2 | US-10-002-750-46 | Sequence 46, Appl |
| 611 | 65 | 5.4 | 176 | 3 | US-10-613-106-5 | Sequence 5, Appli |
| 612 | 65 | 5.4 | 180 | 2 | US-10-002-750-45 | Sequence 45, Appl |
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| 614 | 65 | 5.4 | 181 | 2 | US-09-288-292A-10 | Sequence 10, Appl |
| 615 | 65 | 5.4 | 181 | 2 | US-08-826-246-8 | Sequence 8, Appli |
| 616 | 65 | 5.4 | 182 | 2 | US-08-944-495-8 | Sequence 8, Appli |
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| 624 | 65 | 5.4 | 278 | 2 | US-09-016-8160 | Sequence 8160, Ap |
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| 626 | 65 | 5.4 | 311 | 2 | US-09-252-991A-19489 | Sequence 19489, A |
| 627 | 65 | 5.4 | 322 | 2 | US-09-538-092-506 | Sequence 506, App |
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| 633 | 65 | 5.4 | 375 | 2 | US-09-799-978-6 | Sequence 6, Appli |
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| 636 | 65 | 5.4 | 415 | 2 | US-08-482-746-2 | Sequence 2, Appli |
| 637 | 65 | 5.4 | 415 | 2 | US-08-374-009-2 | Sequence 2, Appli |
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| 640 | 65 | 5.4 | 415 | 3 | US-09-799-978-2 | Sequence 2, Appli |
| 641 | 65 | 5.4 | 415 | 2 | US-09-799-978-4 | Sequence 4, Appli |
| 642 | 65 | 5.4 | 415 | 2 | US-09-799-978-40 | Sequence 40, Appl |
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| 644 | 65 | 5.4 | 432 | 2 | US-09-710-279-780 | Sequence 780, App |
| 645 | 65 | 5.4 | 441 | 2 | US-09-973-025-36 | Sequence 36, Appl |
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| 650 | 65 | 5.4 | 463 | 2 | US-08-927-597-46 | Sequence 46, Appl |
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| 653 | 65 | 5.4 | 490 | 2 | US-09-973-025-46 | Sequence 46, Appl |
| 654 | 65 | 5.4 | 490 | 2 | US-08-612-973-36 | Sequence 36, Appl |
| 655 | 65 | 5.4 | 490 | 2 | US-08-927-597-36 | Sequence 36, Appl |
| 656 | 65 | 5.4 | 490 | 3 | US-08-928-757-36 | Sequence 36, Appl |
| 657 | 65 | 5.4 | 490 | 2 | US-09-973-025-36 | Sequence 36, Appl |
| 658 | 65 | 5.4 | 516 | 2 | US-09-181-339-7 | Sequence 7, Appli |
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| 660 | 65 | 5.4 | 692 | 2 | US-08-612-973-48 | Sequence 48, Appl |
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| 663 | 65 | 5.4 | 692 | 2 | US-09-973-025-48 | Sequence 48, Appl |
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| 682 | 65 | 5.4 | 398 | 2 | US-09-583-110-4666 | Sequence 4666, Ap |
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| 687 | 64.5 | 5.4 | 411 1 | PCT-US95-06725-2 | Sequence 2, Appli |
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| 702 | 64.5 | 5.4 | 476 1 | US-08-855-213-20 | Sequence 20, Appli |
| 703 | 64.5 | 5.4 | 476 1 | US-09-201-474-20 | Sequence 20, Appli |
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| 705 | 64.5 | 5.4 | 482 2 | US-09-134-000C-4234 | Sequence 4234, Ap |
| 706 | 64.5 | 5.4 | 483 2 | US-09-291-922-10 | Sequence 10, Appli |
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| 713 | 64.5 | 5.4 | 495 1 | US-08-855-213-21 | Sequence 21, Appli |
| 714 | 64.5 | 5.4 | 495 2 | US-08-811-897B-5 | Sequence 5, Appli |
| 715 | 64.5 | 5.4 | 495 2 | US-08-947B-16 | Sequence 16, Appli |
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| 717 | 64.5 | 5.4 | 557 2 | US-09-521-195B-27 | Sequence 27, Appli |
| 718 | 64.5 | 5.4 | 557 2 | US-10-172-527A-7 | Sequence 7, Appli |
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| 734 | 64.5 | 5.4 | 216 2 | US-09-270-767-46297 | Sequence 46297, A |
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| 1008 | 62.5 | 5.2 | 796 | 2 | US-08-424-788-5 | Sequence 5, Appli |
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| 1013 | 62.5 | 5.2 | 129 | 2 | US-09-270-767-59183 | Sequence 59183, A |
| 1014 | 62.5 | 5.2 | 238 | 2 | US-09-605-703B-1246 | Sequence 1246, Ap |
| 1015 | 62.5 | 5.2 | 250 | 2 | US-09-673-898-10 | Sequence 10, Appl |
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| 1017 | 62.5 | 5.2 | 272 | 2 | US-09-248-796A-22532 | Sequence 22532, A |
| 1018 | 62.5 | 5.2 | 272 | 2 | US-09-903-456-76 | Sequence 76, Appl |
| 1019 | 62.5 | 5.2 | 272 | 2 | US-09-903-456-80 | Sequence 80, Appl |
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| 1022 | 62.5 | 5.2 | 288 | 2 | US-09-903-456-88 | Sequence 88, Appl |
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| 1025 | 62.5 | 5.2 | 295 | 2 | US-09-903-456-82 | Sequence 82, Appl |
| 1026 | 62.5 | 5.2 | 305 | 2 | US-09-270-767-44944 | Sequence 44944, A |
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| 1045 | 62.5 | 5.2 | 360 | 2 | US-10-101-673-4 | Sequence 4, Appli |
| 1046 | 62.5 | 5.2 | 381 | 3 | US-09-710-279-184 | Sequence 184, Appl |
| 1047 | 62.5 | 5.2 | 384 | 2 | US-09-491-577-16 | Sequence 16, Appl |
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| 1049 | 62 | 5.2 | 405 | 2 | US-09-489-039A-7574 | Sequence 7574, Appli |
| 1050 | 62 | 5.2 | 407 | 2 | US-09-949-016-11348 | Sequence 11348, A |
| 1051 | 62 | 5.2 | 409 | 2 | US-09-583-110-3749 | Sequence 3749, Ap |
| 1052 | 62 | 5.2 | 412 | 2 | US-09-134-001C-3949 | Sequence 3949, Ap |
| 1053 | 62 | 5.2 | 413 | 2 | US-09-107-433-2887 | Sequence 2887, Ap |
| 1054 | 62 | 5.2 | 414 | 2 | US-09-198-452A-414 | Sequence 414, Appl |
| 1055 | 62 | 5.2 | 414 | 2 | US-09-438-185A-396 | Sequence 396, Appl |
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| 1067 | 62 | 5.2 | 489 | 1 | US-09-020-991-24 | Sequence 24, Appl |
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| 1069 | 62 | 5.2 | 489 | 1 | US-09-062-890-22 | Sequence 22, Appl |
| 1070 | 62 | 5.2 | 489 | 1 | US-09-062-890-24 | Sequence 24, Appl |
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| 1077 | 62 | 5.2 | 550 | 2 | US-09-173-151A-24 | Sequence 24, Appl |
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| 1086 | 62 | 5.2 | 638 | 2 | US-09-717-789C-3 | Sequence 3, Appli |
| 1087 | 62 | 5.2 | 687 | 2 | US-09-376-781-6 | Sequence 6, Appli |
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| 1089 | 62 | 5.2 | 747 | 2 | US-09-538-092-957 | Sequence 957, App |
| 1090 | 62 | 5.2 | 775 | 2 | US-09-949-016-10040 | Sequence 10040, A |
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| 1094 | 62 | 5.2 | 1186 | 2 | US-09-668-650-6 | Sequence 6, Appli |
| 1095 | 62 | 5.2 | 1186 | 1 | US-09-543-681A-6130 | Sequence 6130, Ap |
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| 1100 | 61.5 | 5.1 | 170 | 2 | US-09-710-279-1164 | Sequence 1164, Ap |
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| 1116 | 61.5 | 5.1 | 343 | 2 | US-09-875-076-22 | Sequence 22, Appl |
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| 1118 | 61.5 | 5.1 | 350 | 2 | US-09-077-674-3 | Sequence 3, Appli |
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| 1120 | 61.5 | 5.1 | 353 | 2 | US-09-491-577-16 | Sequence 16, Appl |
| 1121 | 61.5 | 5.1 | 361 | 2 | US-09-077-675A-8 | Sequence 8, Appli |

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| 1125 | 61.5 | 5.1 | 366 | 2 | US-09-170-496D-88 | Sequence 88, Appl |
| 1126 | 61.5 | 5.1 | 366 | 2 | US-09-743-742B-7 | Sequence 7, Appli |
| 1127 | 61.5 | 5.1 | 366 | 2 | US-09-762-661A-5 | Sequence 5, Appli |
| 1128 | 61.5 | 5.1 | 366 | 2 | US-09-762-661A-7 | Sequence 7, Appli |
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| 1137 | 61.5 | 5.1 | 379 | 2 | US-10-056-790-40 | Sequence 40, Appli |
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| 1144 | 61.5 | 5.1 | 397 | 2 | US-09-491-577-32 | Sequence 32, Appl |
| 1145 | 61.5 | 5.1 | 411 | 1 | US-09-252-991A-26638 | Sequence 26638, A |
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| 1153 | 61.5 | 5.1 | 415 | 2 | US-08-374-009-6 | Sequence 6, Appli |
| 1154 | 61.5 | 5.1 | 417 | 2 | US-09-799-978-16 | Sequence 16, Appl |
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| 1157 | 61.5 | 5.1 | 458 | 2 | US-08-956-171E-5245 | Sequence 5245, Ap |
| 1158 | 61.5 | 5.1 | 469 | 2 | US-08-781-986A-5245 | Sequence 5245, Ap |
| 1159 | 61.5 | 5.1 | 469 | 1 | US-08-899-514-2 | Sequence 2, Appli |
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| 1161 | 61.5 | 5.1 | 497 | 1 | US-08-633-485-6 | Sequence 6, Appli |
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| 1164 | 61.5 | 5.1 | 510 | 1 | US-09-857-896A-8 | Sequence 8, Appli |
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| 1166 | 61.5 | 5.1 | 526 | 2 | US-08-298-426-4 | Sequence 4, Appli |
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| 1168 | 61.5 | 5.1 | 615 | 2 | US-09-602-787A-536 | Sequence 536, App |
| 1169 | 61.5 | 5.1 | 659 | 2 | US-09-583-110-3110 | Sequence 3110, Ap |
| 1170 | 61.5 | 5.1 | 674 | 2 | US-09-538-092-1125 | Sequence 1125, Ap |
| 1171 | 61.5 | 5.1 | 685 | 2 | US-09-720-317A-31 | Sequence 31, Appl |
| 1172 | 61.5 | 5.1 | 692 | 2 | US-09-248-796A-18612 | Sequence 18612, A |
| 1173 | 61.5 | 5.1 | 756 | 2 | US-09-949-016-6547 | Sequence 6547, Ap |
| 1174 | 61.5 | 1 | 817 | 2 | US-09-381-931B-2 | Sequence 2, Appli |
| 1175 | 61.5 | 5.1 | 865 | 2 | US-09-902-540-10416 | Sequence 10416, A |
| 1176 | 61.5 | 5.1 | 895 | 2 | US-09-489-039A-13127 | Sequence 13127, A |
| 1177 | 61.5 | 5.1 | 965 | 2 | US-09-437-277-3 | Sequence 3, Appli |
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| 1188 | 61.5 | 5.1 | 188 | 2 | US-09-198-452A-1206 | Sequence 1206, Ap |
| 1189 | 61.5 | 5.1 | 189 | 2 | US-08-080-643-4 | Sequence 4, Appli |
| 1190 | 61.5 | 5.1 | 200 | 2 | US-09-710-279-394 | Sequence 394, App |
| 1191 | 61.5 | 5.1 | 200 | 2 | US-09-710-279-1242 | Sequence 1242, Ap |
| 1192 | 61 | 5.1 | 202 | 2 | US-09-657-749D-17 | Sequence 17, Appl |
| 1193 | 61 | 5.1 | 206 | 2 | US-09-134-001C-3929 | Sequence 3929, Ap |
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| 1198 | 61 | 5.1 | 239 | 2 | US-09-710-279-978 | Sequence 978, App |
| 1199 | 61 | 5.1 | 241 | 2 | US-09-489-039A-8397 | Sequence 8397, A |
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| 1210 | 61 | 5.1 | 279 | 2 | US-10-121-857-45 | Sequence 45, Appl |
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| 1212 | 61 | 5.1 | 285 | 2 | US-09-540-236-2583 | Sequence 2583, Ap |
| 1213 | 61 | 5.1 | 296 | 2 | US-09-438-185A-545 | Sequence 545, App |
| 1214 | 61 | 3 | 298 | 2 | US-10-770-127-187 | Sequence 187, App |
| 1215 | 61 | 5.1 | 299 | 2 | US-08-311-731A-173 | Sequence 173, App |
| 1216 | 61 | 5.1 | 302 | 2 | US-10-770-127-187 | Sequence 187, App |
| 1217 | 61 | 5.1 | 338 | 2 | US-09-107-532A-6222 | Sequence 6222, Ap |
| 1218 | 61 | 5.1 | 345 | 2 | US-09-489-039A-5817 | Sequence 5817, Ap |
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ALIGNMENTS

RESULT 1
US-10-104-047-2567
Sequence 2567, Application US/10104047
Patent No. 6943241

; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 694324le1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 2567
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2567

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RESULT 2
US-08-691-814B-6
Sequence 6, Application US/08691814B
Patent No. 5981218

; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Tomasetto, Catherine
; APPLICANT: Basset, Paul
; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave. NW, Suite 600
; CITY: Washington
; STATE: DC

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; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,814B
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,183
; FILING DATE: 09-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1383.0090001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-691-814B-6

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US-09-949-016-8594

RESULT 3
US-09-949-016-8594
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; SEQ ID NO 8594
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; ORGANISM: Human
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US-09-949-016-8594

Query Match    7.2%;    Score 85.5;  DB 2;  Length 449;
Best Local Similarity    25.5%;   Pred. No. 0.49;
Matches 38;  Conservative  18;  Mismatches  46;  Indels  47;  Gaps  8;

Qy  64 LFVTLLWII---------ELNVNGGI-------ENTLEKEVMQYDYSSYFDIFLLAVFRF 108
        :||  | :|        ||:||||        |||||||||||||||||||||||||||
Db 288 VFKGLLWIVPLVVVYFAEYFINGGLFELLFFWNTSLSHAQYRWYQM--LYQAGVFAS 344

Qy 109 KVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFIL----- 163
        :  |  |||||| ||||  | : |     |    |   ||                |
Db 345 R--SSLRCCRIRFTWALALLQCLNLVFLLADV------------WFGF-LPSIYLVFLILY 391

Qy 164 ------AWIETWFLDFKVLPQEAEEENR 185
              :||  : |   | |  ||  |
Db 392 EGLLGGAAYVNT----FHNIALETSDEHR 416
```

```
RESULT 4
US-08-846-762-92
; Sequence 92, Application US/0884676
; Patent No. 5994072
; GENERAL INFORMATION:
; APPLICANT: Lam, Joseph S.
; APPLICANT: Burrows, Lori
; APPLICANT: Charter, Deborah
; APPLICANT: de Kievit, Teresa
; TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
; TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
; FILE REFERENCE: 6580-089
; CURRENT APPLICATION NUMBER: US/08/846,762A
; CURRENT FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 92
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-08-846-762-92

Query Match    6.9%;    Score 82.5;  DB 1;  Length 341;
Best Local Similarity    24.0%;   Pred. No. 0.74;
Matches 31;  Conservative  20;  Mismatches  51;  Indels  27;  Gaps  4;

Qy  47 GISDVRRTFCLFVTFDLLFVTLLMIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVF 106
        | ||  ||| | |  |:  | |    |  ||  |:      |      : |
Db 233 GWIDTRFFCWLIILGLFITVDATWTLVRRVLGGFK------VYEAHRSHG--YQIASR 282

Qy 107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWI 166
        ||| |:|     |||:| |:| |    |   ||    |
Db 283 RFK-------RHLPVTLSAIAINIWLFPIALLAGL-----NIVNPIALIISYI 325

Qy 167 ETWFLDFKV 175
        :|: || |
Db 326 PLLYIDYKL 334
```

```
RESULT 5
US-09-489-039A-9711
; Sequence 9711, Application US/0948903
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9711
```

```
;
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
;

US-09-489-039A-9711

Query Match     6.7%;   Score 80.5;   DB 2;   Length 350;
Best Local Similarity   31.8%;   Pred. No. 1.3;
Matches   21;  Conservative   15;  Mismatches   21;  Indels   9;  Gaps   3;

Qy  111  LILAYAVCRLRHWAIALTTAVTSAFLLAKVILSKL-----FSQGAFGYVLPIISF----IL  163
         :|:|:    :  |: :|  ::|  ::|: :|  ::
Db   83  LLLAVSIPPLAPWMVVLGTAF--AVVIAKQLYGGLGHNPFNPAMIGYVVLLISPPVQMT  140

Qy  164  AWIETW  169
         :| :|:
Db  141  SWLPSY  146

RESULT 6
US-10-226-629A-16
Sequence 16, Application US/10226629A
Patent No. 6960431
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 891
TYPE: PRT
ORGANISM: Vaccinia virus

US-10-226-629A-16

Query Match     6.7%;   Score 80.5;   DB 2;   Length 891;
Best Local Similarity   23.3%;   Pred. No. 4.9;
Matches   38;  Conservative   36;  Mismatches   70;  Indels   19;  Gaps   7;

Qy    7  DMENALTGSQSSHASLRNIHSINPTQLMAR-IESYEGREKKGISDVRRTFCLFVTFDLLF   65
         :  |:|   |:   | : |   :: |||:|   :  |||    |||||||||||||||||
Db  717  NMTNEIT--DMINASLKNTISKDNNMLVSQALNSVANRSKQKIGDLRQSSCKMALLFKNL  774

Qy   66  VTLLWIIELNVNGGIENTLEKEVMQ-YDYY----SSYFDIFLLAVFRFKVLILAYAVCR   119
         |||   |||| :||   |: |   :||| |:|      |||||||||||||||| : |||
Db  775  ATSIYTIERIFANKVGDDVKASMLEKYKVFTDISMSLYKDLIAMENLKAMLYIIRRSGCR  834

Qy  120  LRHWAIALTT-----AVTSAFLLAKVILSKL-----FSQGAFGYV  155
         |||:|:|:|      |  ||||||||||||       ||||||:||
Db  835  IDD--AQITDDLVKSYSLIRPKILSMINYYNEMSRGYFEHM  874
```

```
;
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,699
; FILING DATE: 19-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/015,717
; FILING DATE: 23-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST66APCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-171-699-4

Query Match     6.7%;   Score 79.5;   DB 2;   Length 406;
Best Local Similarity   19.3%;   Pred. No. 2.1;
Matches   52;  Conservative   36;  Mismatches   67;  Indels   115;  Gaps   12;

US-09-171-699-4

Qy   14  GSQSSHASLRNIHSINPTQLMARIESY-----------EGREKKGISDVRRTFCLFVTL   68
         | |||||||||||||||||||      :         ||||||||||||||||
Db  142  GCSQAMALQNLPQCSPDEIMAYAQKIFKLLDEERDK-----------VLTHIDHIFMDI  190

Qy   69  LWIIELNVNGGIENTLEKEVMQYDY-------------YSSYFDIFLLAVFRFKVLILAYAVCRL  120
         |             | :|           |: ||||          :   |||
Db  191  L------------TTCVETMCNEYKVISDACMWTMYGGISLLSEF--------CRV  226

Qy  121  RHWAIALTTAVTSAFLLAK------------------------VLLSKLFSQGAFGYVL-----  156
         :||        |: |||                           |:  ||||||||:||
Db  227  LSCVLEETSV-----MLAKRPLITKPEVISVMKRIEEICMKVPAQ----YILGADPLR  277

Qy  157  ---PIISFILAWIETWFLDFKVLPQEAEENRLLIVQDASERAALIPGGLSDGQFYSPPE  213
Db  278  VCSPSVD----DLRAIAEESDEEAIVAYTLATR------GASSSDSLVSPPE  320

Qy  214  S----------EAGSEEAEEKQDSEK  229
Db  321  SPVPATIPLSSVIVAENSDQEESEQSDEEE  350

RESULT 8
PCT-US94-02107-2
Sequence 2, Application PC/TUS9402107
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of, Anatomy and Biology
TITLE OF INVENTION: Recombinant Cytomegalovirus Vaccine
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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RESULT 7
US-09-171-699-4
Sequence 4, Application US/0917699
Patent No. 6448389
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of, Anatomy & Biology
APPLICANT: Gonczol, Eva
         Berencsi, Klara
         Kari, Csaba
TITLE OF INVENTION: No. 6448389e1 Cytomegalovirus DNA Constructs and
                    Uses Therefor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02107
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/017,130
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST6BPCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-02107-2

Query Match             6.7%;  Score 79.5; DB 5; Length 406;
Best Local Similarity  19.3%;  Pred No. 2.1;
Matches   52;  Conservative   36;  Mismatches   67;  Indels  115;  Gaps  12;

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Qy   14 GSQQSHASLRNHSINPTQLMARIESY------EGREKKGISDVRRTFCLFVTFPLLLFVVTL 68
           |:|:| ||:|:                    |||||::||  ::|  |:|
Db  142 GCSQAMALQNLPQCSPDEIMAYAQKIFKILDEERDK-------------VLTHIDHIFMDI 190

Qy   69 LWIIELNVNGGIENTLEKEVMQYDY----------YSSYFDIFILLAVFRKVLILAYAVCRL 120
Db  191 L--------TTCVETMCNEYKVTSDACMMTMYGGISLLSEF----------CRV 226

Qy  121 RHWWAIALTTAVTSAFLLAK------------------VILSKLFSQGAFGYVL------ 156
Db  227 LSCYVLEETSV-----MLAKRPLITKPEVISVMKRRIEEICMKVFAQ---YILGADPLR 277

Qy  157 ---PIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPE 213
Db  278 VCSPSVD------------DLRAIAEESDEEEAIVAYTLATR-----GASSSDSLVSPPE 320

Qy  214 S----------------EAGSEEAEEKQDSEK 229
Db  321 SPVPATIPLSSVIVAENSDQEESEQSDEEE 350
```

RESULT 9
US-09-976-594-503
; Sequence 503, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 503
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 2246292CD1
US-09-976-594-503

RESULT 10
US-09-270-767-41033
; Sequence 41033, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41033
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41033

Query Match             6.7%;  Score 79.5; DB 2; Length 723;
Best Local Similarity  18.0%;  Pred No. 4.8;
Matches   34;  Conservative   40;  Mismatches   58;  Indels   57;  Gaps   8;

```
Qy   58 FVTFPLLLFVVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFILLAVFRKVLI----- 112
           |:|| |:|::  ||| |:||                      |:|| |:|
Db   13 FMSVDICVTTAIVF---------SHHDRSLLEDIRHFNIFPDSVLDLWAACLYRSCLLIGATIG 67

Qy  113 ----LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ------------------GAFGY 154
Db   68 VAKNSALGPRRLRASWLVISLVCLFVGIYAMVKLL----LFSEVRRPIRDPWFWALFVWTY 124

Qy  155 VLPIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFY----- 209
Db  125 ISLGASFLLWWL-----------------------LSTVRPGTQ-ALEPGAATEAEGFPGSGR 163

Qy  210 SPPESEAGS 218
Db  164 PPPEQASGA 172
```

RESULT 11
US-09-270-767-56249
; Sequence 56249, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56249
; LENGTH: 221

Query Match             6.6%;  Score 78.5; DB 2; Length 221;
Best Local Similarity  22.5%;  Pred No. 1.2;
Matches   38;  Conservative   33;  Mismatches   73;  Indels   25;  Gaps   7;

```
Qy   56 CLFVTFPDL---LFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFILLAVFRKVLI 112
          |::   ||    |:|| |:|| |::| |:|                   |:||  |:||
Db   17 CIYIYSSMDQFLFIIILILILTCLSFVEXYLFVNILLXIDNYIGNXXNVFLFFLLPQXII 76

Qy  113 LAYAVCRLRHWWAIALTT--AVTSAFLLAKVILSKLFSQGAFGYVL-PIISFILAWIETW 169
Db   77 VVVFCCSFCTTYQLIQGTYNSINFRFNLKNLSLT-----LGFLISPPISIHFSYLPHY 129

Qy  170 FLDFKVLPQEAEEENRLL-------IVQDASERAAL--IPGGLSDGQF 208
Db  130 LVNNSVLHLKNVXIQEFLDXVVKCFFILRASFRPCLKDIPNGL--GQF 176
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;    TYPE: PRT
;    ORGANISM: Drosophila melanogaster
;    FEATURE:
;    OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56249

Query Match     6.6%;    Score 78.5;    DB 2;    Length 221;
Best Local Similarity  22.5%;    Pred. No. 1.2;
Matches  38;  Conservative  33;  Mismatches  73;  Indels  25;  Gaps  7;

Qy   56  CLFVTFDL---LFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI 112
             :::|        ::|:| :|::
Db   17  CIVIYSSMDQFLFIIILLILILLTCLSFVEXYLFVNILXIDNYIGNXNVFLFFLLLFQXII 76

Qy  113  LAYAVCLRHWAIALTT--AVTSAFLLAKVILSKLFSQGAPGYVL--PIISFILAWIETW 169
Db   77  VVYFCCSFCTTYQLIQGTYNSINFRFNLKNLSLT------LGFLISPPISIHFSYLPHY 129

Qy  170  FLDFKVLPQEAEEENRLL------IVQDASERAAL--IPGGLSDGQF 208
Db  130  LVNNSVLHLKNVXIQEFLDXVVKCFFILRASFRFCLKDIPNGL--GQF 176


RESULT 12
US-09-724-653-2
;  Sequence 2, Application US/0972465 3
;  Patent No. 6830913
;  GENERAL INFORMATION:
;    APPLICANT: Ling, Victor
;    TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
;    FILE REFERENCE: APZ-004CP
;    CURRENT APPLICATION NUMBER: US/09/724,653
;    CURRENT FILING DATE: 2000-11-28
;    PRIOR APPLICATION NUMBER: 60/167,930
;    PRIOR FILING DATE: 1999-11-29
;    NUMBER OF SEQ ID NOS: 20
;    SOFTWARE: PatentIn Ver. 2.0
;
;    SEQ ID NO 2
;    LENGTH: 766
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-724-653-2

Query Match     6.6%;    Score 78.5;    DB 2;    Length 766;
Best Local Similarity  18.0%;    Pred. No. 6.7;
Matches  34;  Conservative  39;  Mismatches  59;  Indels  57;  Gaps  8;

Qy   58  FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI----- 112
Db   13  FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLGATIG 67

Qy  113  ----LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ--------------GAFGY 154
Db   68  VAKNSALGPRRLRASWLVITLVCLFVGIYAMVKLL---LFSEVRRPIRDPWFWALFVWTY 124

Qy  155  VLPIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFY----- 209
Db  125  ISLGASFLLWML-------------------LSTVRPGTQ--ALEPGAATEAEGPPGSGR 163

Qy  210  SPPESEAGS 218
Db  164  PPPEQASGA 172


RESULT 13
US-09-724-653-14
;  Sequence 14, Application US/0972465 3
;  Patent No. 6830913
;  GENERAL INFORMATION:
;    APPLICANT: Ling, Victor
;    TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
;    FILE REFERENCE: APZ-004CP
;    CURRENT APPLICATION NUMBER: US/09/724,653
;    CURRENT FILING DATE: 2000-11-28
;    PRIOR APPLICATION NUMBER: 60/167,930
;    PRIOR FILING DATE: 1999-11-29
;    NUMBER OF SEQ ID NOS: 20
;    SOFTWARE: PatentIn Ver. 2.0
;
;    SEQ ID NO 14
;    LENGTH: 766
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-724-653-14

Query Match     6.6%;    Score 78.5;    DB 2;    Length 766;
Best Local Similarity  18.0%;    Pred. No. 6.7;
Matches  34;  Conservative  39;  Mismatches  59;  Indels  57;  Gaps  8;

Qy   58  FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI----- 112
Db   13  FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLGATIG 67

Qy  113  ----LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ--------------GAFGY 154
Db   68  VAKNSALGPRRLRASWLVITLVCLFVGIYAMVKLL---LFSEVRRPIRDPWFWALFVWTY 124

Qy  155  VLPIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFY----- 209
Db  125  ISLGASFLLWML-------------------LSTVRPGTQ--ALEPGAATEAEGPPGSGR 163

Qy  210  SPPESEAGS 218
Db  164  PPPEQASGA 172


RESULT 14
US-09-724-653-15
;  Sequence 15, Application US/0972465 3
;  Patent No. 6830913
;  GENERAL INFORMATION:
;    APPLICANT: Ling, Victor
;    TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
;    FILE REFERENCE: APZ-004CP
;    CURRENT APPLICATION NUMBER: US/09/724,653
;    CURRENT FILING DATE: 2000-11-28
;    PRIOR APPLICATION NUMBER: 60/167,930
;    PRIOR FILING DATE: 1999-11-29
;    NUMBER OF SEQ ID NOS: 20
;    SOFTWARE: PatentIn Ver. 2.0
;
;    SEQ ID NO 15
;    LENGTH: 766
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-724-653-15

Query Match     6.6%;    Score 78.5;    DB 2;    Length 766;
Best Local Similarity  18.0%;    Pred. No. 6.7;
Matches  34;  Conservative  39;  Mismatches  59;  Indels  57;  Gaps  8;

Qy   58  FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI----- 112
Db   13  FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLGATIG 67

Qy  113  ----LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ--------------GAFGY 154
Db   68  VAKNSALGPRRLRASWLVITLVCLFVGIYAMVKLL---LFSEVRRPIRDPWFWALFVWTY 124

Qy  155  VLPIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFY----- 209
Db  125  ISLGASFLLWML-------------------LSTVRPGTQ--ALEPGAATEAEGPPGSGR 163

Qy  210  SPPESEAGS 218
Db  164  PPPEQASGA 172
```

RESULT 15
US-09-248-796A-20444
Sequence 20444, Application US/0924879GA
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20444
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-20444

  Query Match             6.5%;   Score 78;  DB 2;  Length 228;
  Best Local Similarity  22.1%;   Pred. No. 1.4;
  Matches   32;  Conservative   32;  Mismatches   49;  Indels   32;  Gaps    7;

Qy         63 LLFVTL-----LWIIELNVN---GGIENTLEKEVMQYDYYSSYF--------DIFLLAVF 106
              :|:|         |:|       |::|           :::|           ||:|
Db         91 LVFFALTSYGAFWLSFAAINIPTFGILAAYQKDMTQLSSALAFYLIAWAILSFIFMLLTF 150

Qy        107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGVVLPIISF----- 161
              :||:|:|:: :     :|::::: : |||||  ::: ::
Db        151 KSTVLLSGFFLC-----LTALFSLLSASYFVGSVALTK--AAGAFGVIAVVAALYDTFA 202

Qy        162 ILAWIETWFLDFKVLP---QEAEEE 183
              :||:|         |:|
Db        203 LLATKQNSYFTLPVIPLPGGSEAKQE 227

Search completed: October 31, 2006, 02:25:23
Job time : 74 secs

OM protein - protein search, using sw model

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GenCore version 5.1.9

Run on: October 31, 2006, 02:32:24 ; Search time 185 Seconds
(without alignments)
585.904 Million cell updates/sec

Sequence: 1 MNHLPEDMENALTGSQSSHA..........EAGSEEAEEKQDSEKPLLEL 234

Perfect score: 1195

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

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SUMMARIES

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| 1136 | 71.5 | 6.0 | 414 | 5 | US-10-732-923-981 | Sequence 981, App |
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| 1138 | 71 | 5.9 | 438 | 6 | US-11-437-004-1118 | Sequence 1118, Ap |
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| 1170 | 71 | 5.9 | 629 | 6 | US-10-437-963-119462 | Sequence 119462, |
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| 1263 | 70.5 | 5.9 | 333 | 4 | US-10-225-567A-279 | Sequence 279, App |
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| 90 | 73 | 6.1 | 249 | 7 | US-11-434-199-7910 | Sequence 7910, Ap |
| 91 | 73 | 6.1 | 249 | 7 | US-11-434-203-7910 | Sequence 7910, Ap |
| 92 | 73 | 6.1 | 290 | 6 | US-10-471-571A-4788 | Sequence 4788, Ap |
| 93 | 73 | 6.1 | 415 | 7 | US-11-056-355B-82151 | Sequence 82151, A |
| 94 | 73 | 6.1 | 472 | 7 | US-11-056-355B-82150 | Sequence 82150, A |
| 95 | 73 | 6.1 | 474 | 7 | US-11-056-355B-82149 | Sequence 82149, A |
| 96 | 73 | 6.1 | 474 | 7 | US-11-330-403-16009 | Sequence 16009, A |
| 97 | 73 | 6.1 | 494 | 7 | US-10-449-902-54489 | Sequence 54489, A |
| 98 | 73 | 6.1 | 494 | 6 | US-10-251-145-17 | Sequence 17, Appl |
| 99 | 73 | 6.1 | 792 | 6 | US-10-471-571A-4714 | Sequence 4714, Ap |
| 100 | 73 | 6.1 | 1314 | 6 | US-10-449-902-41194 | Sequence 41194, A |

| 101 | 72.5 | 6.1 | 209 | 6 | US-10-953-349-2299 | Sequence 2299, Ap |
| 102 | 72.5 | 6.1 | 209 | 7 | US-11-056-355B-40232 | Sequence 40232, A |
| 103 | 72.5 | 6.1 | 209 | 7 | US-11-056-355B-103777 | Sequence 103777, |
| 104 | 72.5 | 6.1 | 209 | 7 | US-11-056-355B-115016 | Sequence 115016, |
| 105 | 72.5 | 6.1 | 216 | 7 | US-11-056-355B-103776 | Sequence 103776, |
| 106 | 72.5 | 6.1 | 216 | 7 | US-11-056-355B-115015 | Sequence 115015, |
| 107 | 72.5 | 6.1 | 278 | 7 | US-11-330-403-9646 | Sequence 9646, Ap |
| 108 | 72.5 | 6.1 | 291 | 7 | US-11-056-355B-7634 | Sequence 7634, Ap |
| 109 | 72.5 | 6.1 | 291 | 7 | US-11-305-666-67 | Sequence 67, Appl |
| 110 | 72.5 | 6.1 | 291 | 7 | US-11-305-666-86 | Sequence 86, Appl |
| 111 | 72.5 | 6.1 | 291 | 7 | US-11-305-666-87 | Sequence 87, Appl |
| 112 | 72.5 | 6.1 | 291 | 7 | US-11-305-666-88 | Sequence 88, Appl |
| 113 | 72.5 | 6.1 | 306 | 7 | US-11-056-355B-7633 | Sequence 7633, Ap |
| 114 | 72.5 | 6.1 | 389 | 6 | US-11-565-487-1 | Sequence 1, Appli |
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| 116 | 72.5 | 6.1 | 740 | 6 | US-10-449-902-55531 | Sequence 55531, A |
| 117 | 72.5 | 6.1 | 378 | 6 | US-11-669-920-493 | Sequence 493, App |
| 118 | 72.5 | 6.1 | 378 | 6 | US-11-669-920-495 | Sequence 495, App |
| 119 | 72.5 | 6.1 | 398 | 7 | US-11-056-355B-90585 | Sequence 90585, A |
| 120 | 72 | 6.0 | 398 | 7 | US-10-523-593-94341 | Sequence 94341, A |
| 121 | 72 | 6.0 | 447 | 6 | US-11-471-571A-4130 | Sequence 4130, Ap |
| 122 | 72 | 6.0 | 461 | 7 | US-11-056-355B-90584 | Sequence 90584, A |
| 123 | 72 | 6.0 | 461 | 7 | US-11-056-355B-94340 | Sequence 94340, A |
| 124 | 72 | 6.0 | 468 | 7 | US-11-056-355B-90583 | Sequence 90583, A |
| 125 | 72 | 6.0 | 495 | 7 | US-11-056-355B-94339 | Sequence 94339, A |
| 126 | 72 | 6.0 | 468 | 7 | US-11-056-355B-6931 | Sequence 6931, Ap |
| 127 | 72 | 6.0 | 497 | 7 | US-10-953-349-6930 | Sequence 6930, Ap |
| 128 | 72 | 6.0 | 507 | 6 | US-10-953-349-6929 | Sequence 6929, Ap |
| 129 | 72 | 6.0 | 742 | 6 | US-11-518-941-26 | Sequence 26, Appl |
| 130 | 72 | 6.0 | 746 | 6 | US-11-056-355B-4287 | Sequence 4287, Ap |
| 131 | 71.5 | 6.0 | 218 | 7 | US-11-056-355B-23091 | Sequence 23091, A |
| 132 | 71.5 | 6.0 | 472 | 7 | US-11-056-355B-72423 | Sequence 72423, A |
| 133 | 71.5 | 6.0 | 491 | 7 | US-11-056-355B-72422 | Sequence 72422, A |
| 134 | 71.5 | 6.0 | 510 | 7 | US-11-330-403-17869 | Sequence 17869, A |
| 135 | 71.5 | 6.0 | 603 | 6 | US-11-471-571A-3718 | Sequence 3718, Ap |
| 136 | 71.5 | 6.0 | 651 | 6 | US-11-056-355B-72421 | Sequence 72421, A |
| 137 | 71.5 | 6.0 | 890 | 6 | US-10-570-909-67 | Sequence 67, Appl |
| 138 | 71.5 | 6.0 | 2923 | 6 | US-10-570-909-35 | Sequence 35, Appl |
| 139 | 71.5 | 6.0 | 2923 | 6 | US-10-570-909-39 | Sequence 39, Appl |
| 140 | 71 | 6.0 | 276 | 7 | US-11-056-355B-44017 | Sequence 44017, A |
| 141 | 71 | 6.0 | 290 | 7 | US-11-056-355B-44016 | Sequence 44016, A |
| 142 | 71 | 6.0 | 295 | 7 | US-11-434-184-1686 | Sequence 1686, Ap |
| 143 | 71 | 6.0 | 295 | 7 | US-11-434-199-1686 | Sequence 1686, Ap |
| 144 | 71 | 6.0 | 295 | 7 | US-11-434-203-1686 | Sequence 1686, Ap |
| 145 | 71 | 6.0 | 295 | 7 | US-11-434-207B-1686 | Sequence 1686, Ap |
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| 147 | 71 | 6.0 | 483 | 7 | US-11-174-307B-5500 | Sequence 5500, Ap |
| 148 | 71 | 6.0 | 495 | 7 | US-10-449-902-32757 | Sequence 32757, A |
| 149 | 71 | 6.0 | 495 | 7 | US-10-449-902-43122 | Sequence 43122, A |
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| 155 | 71 | 6.0 | 676 | 7 | US-11-056-355B-69511 | Sequence 69511, A |
| 156 | 71 | 6.0 | 825 | 7 | US-11-056-355B-69915 | Sequence 69915, A |
| 157 | 71 | 6.0 | 826 | 7 | US-11-056-355B-69914 | Sequence 69914, A |
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| 159 | 70.5 | 6.0 | 402 | 6 | US-10-530-187-264 | Sequence 264, App |
| 160 | 70.5 | 6.0 | 620 | 7 | US-11-056-355B-88722 | Sequence 88722, A |
| 161 | 70.5 | 6.0 | 620 | 7 | US-11-056-355B-92478 | Sequence 92478, A |
| 162 | 70.5 | 6.0 | 622 | 7 | US-11-056-355B-88721 | Sequence 88721, A |
| 163 | 70.5 | 6.0 | 623 | 7 | US-11-056-355B-92477 | Sequence 92477, A |
| 164 | 70.5 | 6.0 | 625 | 7 | US-11-056-355B-70840 | Sequence 70840, A |
| 165 | 70.5 | 6.0 | 697 | 7 | US-11-056-355B-70839 | Sequence 70839, A |
| 166 | 70.5 | 6.0 | 697 | 7 | US-11-056-355B-88720 | Sequence 88720, A |
| 167 | 70.5 | 6.0 | 700 | 7 | US-11-056-355B-92476 | Sequence 92476, A |
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| 169 | 70 | 5.9 | 185 | 7 | US-11-056-355B-26745 | Sequence 26745, A |
| 170 | 70 | 5.9 | 185 | 7 | US-11-056-355B-30003 | Sequence 30003, A |
| 171 | 70 | 5.9 | 185 | 7 | US-11-056-355B-33593 | Sequence 33593, A |
| 172 | 70 | 5.9 | 189 | 7 | US-11-056-355B-26744 | Sequence 26744, A |
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| 174 | 70 | 5.9 | 189 | 7 | US-11-056-355B-33592 | Sequence 33592, A |
| 175 | 70 | 5.9 | 235 | 7 | US-11-056-355B-26743 | Sequence 26743, A |
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| 177 | 70 | 5.9 | 235 | 7 | US-11-056-355B-33591 | Sequence 33591, A |
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| 179 | 70 | 5.9 | 274 | 7 | US-11-056-355B-76301 | Sequence 76301, A |
| 180 | 70 | 5.9 | 274 | 7 | US-11-056-355B-77453 | Sequence 77453, A |
| 181 | 70 | 5.9 | 274 | 7 | US-11-056-355B-104540 | Sequence 104540, |
| 182 | 70 | 5.9 | 274 | 7 | US-11-056-355B-115779 | Sequence 115779, |
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| 184 | 70 | 5.9 | 287 | 7 | US-11-056-355B-76300 | Sequence 76300, A |
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| 186 | 70 | 5.9 | 287 | 7 | US-11-056-355B-104539 | Sequence 104539, |
| 187 | 70 | 5.9 | 287 | 7 | US-11-056-355B-115778 | Sequence 115778, |
| 188 | 70 | 5.9 | 367 | 7 | US-11-056-355B-3278 | Sequence 3278, Ap |
| 189 | 70 | 5.9 | 383 | 7 | US-11-056-355B-3277 | Sequence 3277, Ap |
| 190 | 70 | 5.9 | 475 | 7 | US-10-953-349-17159 | Sequence 17159, A |
| 191 | 70 | 5.9 | 475 | 7 | US-11-056-355B-53799 | Sequence 53799, A |
| 192 | 70 | 5.9 | 506 | 7 | US-10-471-571A-3308 | Sequence 3308, Ap |
| 193 | 69.5 | 5.9 | 532 | 7 | US-10-523-593-16523 | Sequence 16523, A |
| 194 | 69.5 | 5.9 | 206 | 7 | US-10-953-349-15493 | Sequence 15493, A |
| 195 | 69.5 | 5.9 | 317 | 7 | US-11-056-355B-91422 | Sequence 91422, A |
| 196 | 69.5 | 5.9 | 317 | 7 | US-11-056-355B-95178 | Sequence 95178, A |
| 197 | 69.5 | 5.8 | 354 | 7 | US-11-056-032-12 | Sequence 12, Appl |
| 198 | 69.5 | 5.8 | 371 | 7 | US-11-056-355B-9101 | Sequence 9101, Ap |
| 199 | 69.5 | 5.8 | 381 | 7 | US-11-056-355B-9100 | Sequence 9100, Ap |
| 200 | 69.5 | 5.8 | 430 | 7 | US-11-056-355B-9099 | Sequence 9099, Ap |
| 201 | 69.5 | 5.8 | 453 | 7 | US-11-330-403-8969 | Sequence 8969, Ap |
| 202 | 69.5 | 5.8 | 476 | 7 | US-11-056-355B-91576 | Sequence 91576, A |
| 203 | 69.5 | 5.8 | 476 | 7 | US-11-056-355B-95332 | Sequence 95332, A |
| 204 | 69.5 | 5.8 | 503 | 7 | US-11-056-355B-91575 | Sequence 91575, A |
| 205 | 69.5 | 5.8 | 503 | 7 | US-11-056-355B-95331 | Sequence 95331, A |
| 206 | 69.5 | 5.8 | 534 | 7 | US-11-056-355B-91574 | Sequence 91574, A |
| 207 | 69.5 | 5.8 | 534 | 7 | US-11-056-355B-95330 | Sequence 95330, A |
| 208 | 69.5 | 5.8 | 557 | 7 | US-11-330-813-4 | Sequence 4, Appli |
| 209 | 69.5 | 5.8 | 584 | 7 | US-11-330-403-17971 | Sequence 17971, A |
| 210 | 69.5 | 5.8 | 599 | 6 | US-11-302-678-5 | Sequence 5, Appli |
| 211 | 69.5 | 5.8 | 1704 | 6 | US-10-570-909-103 | Sequence 103, Appl |
| 212 | 69.5 | 5.8 | 1704 | 6 | US-11-289-102-341 | Sequence 341, App |
| 213 | 69 | 5.8 | 200 | 7 | US-11-056-355B-71812 | Sequence 71812, A |
| 214 | 69 | 5.8 | 214 | 7 | US-11-293-697-2534 | Sequence 2534, Ap |
| 215 | 69 | 5.8 | 252 | 7 | US-11-056-355B-71811 | Sequence 71811, A |
| 216 | 69 | 5.8 | 290 | 7 | US-11-305-666-65 | Sequence 65, Appl |
| 217 | 69 | 5.8 | 290 | 7 | US-11-305-666-83 | Sequence 83, Appl |
| 218 | 69 | 5.8 | 326 | 7 | US-11-056-355B-71810 | Sequence 71810, A |
| 219 | 69 | 5.8 | 350 | 6 | US-11-471-571A-4042 | Sequence 4042, Ap |
| 220 | 69 | 5.8 | 350 | 7 | US-10-449-902-50010 | Sequence 50010, A |
| 221 | 69 | 5.8 | 440 | 7 | US-10-953-349-22057 | Sequence 22057, A |
| 222 | 69 | 5.8 | 440 | 7 | US-10-953-349-22056 | Sequence 22056, A |
| 223 | 69 | 5.8 | 450 | 7 | US-11-056-355B-58390 | Sequence 58390, A |
| 224 | 69 | 5.8 | 450 | 7 | US-11-056-355B-58389 | Sequence 58389, A |
| 225 | 69 | 5.8 | 508 | 7 | US-10-953-349-5613 | Sequence 5613, Ap |
| 226 | 69 | 5.8 | 508 | 7 | US-10-953-349-5612 | Sequence 5612, Ap |
| 227 | 69 | 5.8 | 520 | 7 | US-11-056-355B-36302 | Sequence 36302, A |
| 228 | 69 | 5.8 | 520 | 7 | US-11-056-355B-36301 | Sequence 36301, A |
| 229 | 69 | 5.8 | 526 | 7 | US-11-330-403-9817 | Sequence 9817, Ap |
| 230 | 69 | 5.8 | 526 | 7 | US-11-024-544A-12 | Sequence 12, Appl |
| 231 | 69 | 5.8 | 526 | 7 | US-11-024-544A-14 | Sequence 14, Appl |
| 232 | 69 | 5.8 | 526 | 7 | US-11-190-750-80 | Sequence 80, Appl |
| 233 | 69 | 5.8 | 526 | 7 | US-11-190-750-84 | Sequence 84, Appl |
| 234 | 69 | 5.8 | 526 | 7 | US-11-264-784-82 | Sequence 82, Appl |
| 235 | 69 | 5.8 | 526 | 7 | US-11-265-761-95 | Sequence 95, Appl |
| 236 | 69 | 5.8 | 526 | 7 | US-11-264-721-123 | Sequence 123, App |
| 237 | 69 | 5.8 | 526 | 7 | US-10-449-902-48588 | Sequence 48588, A |
| 238 | 69 | 5.8 | 569 | 6 | US-10-449-902-36835 | Sequence 36835, A |
| 239 | 69 | 5.8 | 569 | 6 | US-10-449-902-50106 | Sequence 50106, A |
| 240 | 69 | 5.8 | 569 | 6 | US-10-449-902-50472 | Sequence 50472, A |
| 241 | 69 | 5.8 | 647 | 6 | US-11-330-403-5831 | Sequence 5831, Ap |
| 242 | 68.5 | 5.8 | 211 | 7 | US-11-199-489A-94 | Sequence 94, Appl |
| 243 | 68.5 | 5.8 | 218 | 7 | US-11-056-355B-72029 | Sequence 72029, A |
| 244 | 68.5 | 5.7 | 243 | 7 | US-11-056-355B-91424 | Sequence 91424, A |
| 245 | 68.5 | 5.7 | 245 | 7 | US-11-056-355B-95180 | Sequence 95180, A |
| 246 | 68.5 | 5.7 | 227 | 7 | US-11-333-747A-144 | Sequence 144, App |

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| 247 | 68.5 | 5.7 | 228 | 7 | US-11-305-666-77 | Sequence 77, Appl |
| 248 | 68.5 | 5.7 | 233 | 7 | US-11-056-355B-91423 | Sequence 91423, A |
| 249 | 68.5 | 5.7 | 233 | 7 | US-11-056-355B-95179 | Sequence 95179, A |
| 250 | 68.5 | 5.7 | 287 | 7 | US-11-305-666-85 | Sequence 85, Appl |
| 251 | 68.5 | 5.7 | 378 | 6 | US-10-669-920-490 | Sequence 490, Appl |
| 252 | 68.5 | 5.7 | 435 | 7 | US-11-056-355B-91465 | Sequence 91465, A |
| 253 | 68.5 | 5.7 | 435 | 7 | US-11-056-355B-95221 | Sequence 95221, A |
| 254 | 68.5 | 5.7 | 444 | 7 | US-11-358-841-2 | Sequence 2, Appli |
| 255 | 68.5 | 5.7 | 468 | 7 | US-11-404-939-553 | Sequence 553, App |
| 256 | 68.5 | 5.7 | 500 | 7 | US-11-056-355B-91464 | Sequence 91464, A |
| 257 | 68.5 | 5.7 | 500 | 7 | US-11-056-355B-95220 | Sequence 95220, A |
| 258 | 68.5 | 5.6 | 501 | 6 | US-10-449-902-46991 | Sequence 46991, A |
| 259 | 68.5 | 5.7 | 501 | 7 | US-11-056-355B-91477 | Sequence 91477, A |
| 260 | 68.5 | 5.7 | 516 | 7 | US-11-056-355B-95233 | Sequence 95233, A |
| 261 | 68.5 | 5.7 | 528 | 7 | US-11-056-355B-79431 | Sequence 79431, A |
| 262 | 68.5 | 5.7 | 590 | 7 | US-11-056-355B-79430 | Sequence 79430, A |
| 263 | 68.5 | 5.7 | 643 | 7 | US-11-056-355B-91476 | Sequence 91476, A |
| 264 | 68.5 | 5.7 | 643 | 7 | US-11-056-355B-95232 | Sequence 95232, A |
| 265 | 68.5 | 5.7 | 894 | 7 | US-11-056-355B-91475 | Sequence 91475, A |
| 266 | 68.5 | 5.7 | 894 | 7 | US-11-056-355B-95231 | Sequence 95231, A |
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| 268 | 68.5 | 5.7 | 894 | 7 | US-11-056-355B-5482 | Sequence 5482, Ap |
| 269 | 68.5 | 5.7 | 894 | 7 | US-11-056-355B-8898 | Sequence 8898, Ap |
| 270 | 68.5 | 5.7 | 894 | 7 | US-11-434-137-5482 | Sequence 5482, Ap |
| 271 | 68.5 | 5.7 | 894 | 7 | US-11-434-184-8898 | Sequence 8898, Ap |
| 272 | 68.5 | 5.7 | 344 | 7 | US-11-434-199-5482 | Sequence 5482, Ap |
| 273 | 68.5 | 5.7 | 643 | 7 | US-11-056-355B-91476 | Sequence 91476, A |
| 274 | 68.5 | 5.7 | 894 | 7 | US-11-434-203-5482 | Sequence 5482, Ap |
| 275 | 68.5 | 5.7 | 894 | 7 | US-11-056-355B-8898 | Sequence 8898, Ap |
| 276 | 68.5 | 5.7 | 247 | 7 | US-11-805-394-5109 | Sequence 5109, Ap |
| 277 | 68.5 | 5.7 | 295 | 7 | US-11-293-697-4304 | Sequence 4304, Ap |
| 278 | 68 | 5.7 | 312 | 6 | US-10-449-902-43616 | Sequence 43616, A |
| 279 | 68 | 5.7 | 330 | 6 | US-10-953-349-5614 | Sequence 5614, Ap |
| 280 | 68 | 5.7 | 330 | 7 | US-11-056-355B-23626 | Sequence 23626, A |
| 281 | 68 | 5.7 | 330 | 7 | US-11-434-203-396 | Sequence 396, Ap |
| 282 | 68 | 5.7 | 346 | 7 | US-11-403-051-30 | Sequence 30, Appl |
| 283 | 68 | 5.7 | 341 | 7 | US-11-403-051-2 | Sequence 2, Appli |
| 284 | 68 | 5.7 | 342 | 6 | US-11-403-051-55 | Sequence 55, Appl |
| 285 | 68 | 5.7 | 344 | 6 | US-10-449-902-43901 | Sequence 43901, A |
| 286 | 68 | 5.7 | 344 | 7 | US-11-434-137-396 | Sequence 396, Ap |
| 287 | 68 | 5.7 | 344 | 7 | US-11-434-184-396 | Sequence 396, App |
| 288 | 68 | 5.7 | 344 | 7 | US-11-434-199-396 | Sequence 396, Ap |
| 289 | 68 | 5.7 | 346 | 7 | US-11-434-203-396 | Sequence 396, Ap |
| 290 | 68 | 5.7 | 346 | 7 | US-11-403-149-30 | Sequence 30, Appl |
| 291 | 68 | 5.7 | 355 | 7 | US-11-363-151-84 | Sequence 84, Appl |
| 292 | 68 | 5.7 | 388 | 7 | US-11-363-149-84 | Sequence 84, Appl |
| 293 | 68 | 5.7 | 388 | 6 | US-10-449-902-49827 | Sequence 49827, A |
| 294 | 68 | 5.7 | 488 | 6 | US-11-404-939-561 | Sequence 561, App |
| 295 | 68 | 5.7 | 689 | 6 | US-10-449-902-45629 | Sequence 45629, A |
| 296 | 68 | 5.7 | 689 | 6 | US-11-449-902-47834 | Sequence 47834, A |
| 297 | 68 | 5.7 | 694 | 7 | US-11-056-355B-72708 | Sequence 72708, A |
| 298 | 68 | 5.7 | 710 | 7 | US-11-056-355B-72706 | Sequence 72706, A |
| 299 | 68 | 5.7 | 804 | 7 | US-11-056-355B-72707 | Sequence 72707, A |
| 300 | 68 | 5.7 | 1575 | 6 | US-10-543-503-134 | Sequence 134, App |
| 301 | 68 | 5.7 | 2359 | 6 | US-10-449-902-50506 | Sequence 50506, A |
| 302 | 68 | 5.7 | 3010 | 7 | US-11-140-487A-769 | Sequence 769, App |
| 303 | 68 | 5.7 | 3010 | 7 | US-11-140-487A-770 | Sequence 770, App |
| 304 | 67.5 | 5.6 | 213 | 7 | US-11-056-355B-23092 | Sequence 23092, A |
| 305 | 67.5 | 5.6 | 250 | 6 | US-11-056-355B-49321 | Sequence 49321, A |
| 306 | 67.5 | 5.6 | 286 | 7 | US-11-056-355B-51767 | Sequence 51767, A |
| 307 | 67.5 | 5.6 | 286 | 7 | US-11-056-355B-64 | Sequence 64, Appl |
| 308 | 67.5 | 5.6 | 292 | 7 | US-11-056-355B-82 | Sequence 82, Appl |
| 309 | 67.5 | 5.6 | 321 | 7 | US-11-056-355B-11206 | Sequence 11206, A |
| 310 | 67.5 | 5.6 | 348 | 6 | US-11-449-902-43070 | Sequence 43070, A |
| 311 | 67.5 | 5.6 | 354 | 7 | US-11-056-355B-11205 | Sequence 11205, A |
| 312 | 67.5 | 5.6 | 387 | 7 | US-11-056-355B-11205 | Sequence 11205, A |
| 313 | 67.5 | 5.6 | 387 | 7 | US-11-107-336-44 | Sequence 44, Appl |
| 314 | 67.5 | 5.6 | 431 | 7 | US-11-434-137-3244 | Sequence 3244, Ap |
| 315 | 67.5 | 5.6 | 431 | 7 | US-11-434-184-3244 | Sequence 3244, Ap |
| 316 | 67.5 | 5.6 | 431 | 7 | US-11-434-199-3244 | Sequence 3244, Ap |
| 317 | 67.5 | 5.6 | 431 | 7 | US-11-434-203-3244 | Sequence 3244, Ap |
| 318 | 67.5 | 5.6 | 534 | 7 | US-11-434-137-2878 | Sequence 2878, Ap |
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| 320 | 67.5 | 5.6 | 534 | 7 | US-11-434-199-2878 | Sequence 2878, Ap |
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| 322 | 67.5 | 5.6 | 608 | 7 | US-11-293-697-4385 | Sequence 4385, Ap |
| 323 | 67.5 | 5.6 | 933 | 7 | US-11-248-718-138 | Sequence 138, App |
| 324 | 67.5 | 5.6 | 933 | 7 | US-11-226-554-138 | Sequence 138, App |
| 325 | 67 | 5.6 | 158 | 7 | US-11-434-203-3540 | Sequence 3540, Ap |
| 326 | 67 | 5.6 | 158 | 7 | US-11-434-718-2484 | Sequence 2484, Ap |
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| 1041 | 61.5 | 5.1 | 207 | 7 | US-11-434-199-9874 | Sequence 9874, Ap |
| 1042 | 61.5 | 5.1 | 207 | 7 | US-11-434-184-9874 | Sequence 9874, Ap |
| 1043 | 61.5 | 5.1 | 207 | 7 | US-11-434-203-9874 | Sequence 9874, Ap |
| 1044 | 61.5 | 5.1 | 212 | 7 | US-11-434-137-2812 | Sequence 2812, Ap |
| 1045 | 61.5 | 5.1 | 212 | 7 | US-11-434-184-2812 | Sequence 2812, Ap |
| 1046 | 61.5 | 5.1 | 212 | 7 | US-11-434-199-2812 | Sequence 2812, Ap |
| 1047 | 61.5 | 5.1 | 212 | 7 | US-11-434-203-2812 | Sequence 2812, Ap |
| 1048 | 61 | 5.1 | 219 | 6 | US-10-535-928A-33 | Sequence 33, Appl |
| 1049 | 61 | 5.1 | 228 | 7 | US-11-434-137-6808 | Sequence 6808, Ap |
| 1050 | 61 | 5.1 | 228 | 7 | US-11-434-184-6808 | Sequence 6808, Ap |
| 1051 | 61 | 5.1 | 228 | 7 | US-11-434-199-6808 | Sequence 6808, Ap |

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| 1052 | 61 | 5.1 | 228 | 7 | US-11-434-203-6808 | Sequence 6808, Ap |
| 1053 | 61 | 5.1 | 243 | 7 | US-11-056-355B-59224 | Sequence 59224, A |
| 1054 | 61 | 5.1 | 256 | 6 | US-10-623-808-6 | Sequence 6, Appli |
| 1055 | 61 | 5.1 | 256 | 7 | US-11-128-422-6 | Sequence 6, Appli |
| 1056 | 61 | 5.1 | 276 | 7 | US-10-370-754-5 | Sequence 5, Appli |
| 1057 | 61 | 5.1 | 288 | 7 | US-10-449-902-40104 | Sequence 40104, A |
| 1058 | 61 | 5.1 | 288 | 7 | US-11-056-355B-59223 | Sequence 59223, A |
| 1059 | 61 | 5.1 | 289 | 7 | US-11-056-355B-5753 | Sequence 5753, Ap |
| 1060 | 61 | 5.1 | 299 | 7 | US-11-375-359-134 | Sequence 134, App |
| 1061 | 61 | 5.1 | 299 | 7 | US-11-073-360-195 | Sequence 195, App |
| 1062 | 61 | 5.1 | 301 | 6 | US-10-449-902-55919 | Sequence 55919, A |
| 1063 | 61 | 5.1 | 303 | 7 | US-10-953-349-4315 | Sequence 4315, Ap |
| 1064 | 61 | 5.1 | 310 | 7 | US-10-953-349-4316 | Sequence 4316, Ap |
| 1065 | 61 | 5.1 | 312 | 7 | US-11-140-450-59 | Sequence 59, Appl |
| 1066 | 61 | 5.1 | 315 | 6 | US-10-953-349-4314 | Sequence 4314, Ap |
| 1067 | 61 | 5.1 | 324 | 7 | US-11-056-355B-103484 | Sequence 103484, |
| 1068 | 61 | 5.1 | 324 | 7 | US-11-056-355B-114723 | Sequence 114723, |
| 1069 | 61 | 5.1 | 332 | 7 | US-11-056-355B-38710 | Sequence 38710, A |
| 1070 | 61 | 5.1 | 334 | 7 | US-11-056-355B-97222 | Sequence 97222, A |
| 1071 | 61 | 5.1 | 338 | 7 | US-11-056-355B-59222 | Sequence 59222, A |
| 1072 | 61 | 5.1 | 343 | 7 | US-11-056-355B-38709 | Sequence 38709, A |
| 1073 | 61 | 5.1 | 347 | 6 | US-11-056-355B-103483 | Sequence 103483, |
| 1074 | 61 | 5.1 | 347 | 7 | US-11-056-355B-114722 | Sequence 114722, |
| 1075 | 61 | 5.1 | 363 | 7 | US-11-056-355B-38708 | Sequence 38708, A |
| 1076 | 61 | 5.1 | 377 | 6 | US-10-953-349-12021 | Sequence 12021, A |
| 1077 | 61 | 5.1 | 392 | 7 | US-11-056-355B-103482 | Sequence 103482, |
| 1078 | 61 | 5.1 | 392 | 7 | US-11-056-355B-114721 | Sequence 114721, |
| 1079 | 61 | 5.1 | 398 | 7 | US-11-330-403-13236 | Sequence 13236, A |
| 1080 | 61 | 5.1 | 407 | 7 | US-11-366-965-273 | Sequence 273, App |
| 1081 | 61 | 5.1 | 414 | 7 | US-10-805-394-6146 | Sequence 6146, Ap |
| 1082 | 61 | 5.1 | 417 | 7 | US-11-056-355B-77908 | Sequence 77908, A |
| 1083 | 61 | 5.1 | 421 | 7 | US-11-056-355B-97221 | Sequence 97221, A |
| 1084 | 61 | 5.1 | 425 | 7 | US-11-056-355B-14012 | Sequence 14012, A |
| 1085 | 61 | 5.1 | 431 | 6 | US-10-449-902-43427 | Sequence 43427, A |
| 1086 | 61 | 5.1 | 445 | 7 | US-11-412-025-34 | Sequence 34, Appl |
| 1087 | 61 | 5.1 | 453 | 7 | US-11-056-355B-77907 | Sequence 77907, A |
| 1088 | 61 | 5.1 | 470 | 7 | US-11-449-902-54892 | Sequence 54892, A |
| 1089 | 61 | 5.1 | 485 | 7 | US-11-056-355B-77906 | Sequence 77906, A |
| 1090 | 61 | 5.1 | 485 | 7 | US-11-409-453-4 | Sequence 4, Appli |
| 1091 | 61 | 5.1 | 519 | 7 | US-11-409-530-4 | Sequence 4, Appli |
| 1092 | 61 | 5.1 | 521 | 7 | US-11-056-355B-2396 | Sequence 2396, Ap |
| 1093 | 61 | 5.1 | 527 | 7 | US-11-056-355B-97220 | Sequence 97220, A |
| 1094 | 61 | 5.1 | 548 | 7 | US-11-056-355B-2394 | Sequence 2394, Ap |
| 1095 | 61 | 5.1 | 611 | 6 | US-10-540-898-553 | Sequence 553, App |
| 1096 | 61 | 5.1 | 621 | 7 | US-11-056-355B-90068 | Sequence 90068, A |
| 1097 | 61 | 5.1 | 621 | 7 | US-11-056-355B-93824 | Sequence 93824, A |
| 1098 | 61 | 5.1 | 621 | 7 | US-11-056-355B-107831 | Sequence 107831, |
| 1099 | 61 | 5.1 | 621 | 7 | US-11-056-355B-119070 | Sequence 119070, |
| 1100 | 61 | 5.1 | 632 | 6 | US-11-056-355B-14011 | Sequence 14011, A |
| 1101 | 61 | 5.1 | 632 | 6 | US-10-449-902-51656 | Sequence 51656, A |
| 1102 | 61 | 5.1 | 677 | 7 | US-11-056-355B-80397 | Sequence 80397, A |
| 1103 | 61 | 5.1 | 683 | 7 | US-11-056-355B-80396 | Sequence 80396, A |
| 1104 | 61 | 5.1 | 683 | 7 | US-11-527-422-15 | Sequence 15, Appl |
| 1105 | 61 | 5.1 | 693 | 7 | US-11-056-355B-80395 | Sequence 80395, A |
| 1106 | 61 | 5.1 | 712 | 7 | US-10-953-349-14010 | Sequence 14010, A |
| 1107 | 61 | 5.1 | 774 | 7 | US-10-953-349-38348 | Sequence 38348, A |
| 1108 | 61 | 5.1 | 779 | 7 | US-10-953-349-38347 | Sequence 38347, A |
| 1109 | 61 | 5.1 | 790 | 6 | US-11-449-902-47109 | Sequence 47109, A |
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| 1111 | 61 | 5.1 | 793 | 6 | US-11-434-137-4172 | Sequence 4172, Ap |
| 1112 | 61 | 5.1 | 893 | 7 | US-11-434-199-4172 | Sequence 4172, Ap |
| 1113 | 61 | 5.1 | 893 | 7 | US-11-434-203-4172 | Sequence 4172, Ap |
| 1114 | 61 | 5.1 | 893 | 7 | US-10-539-228-693 | Sequence 693, App |
| 1115 | 61 | 5.1 | 911 | 7 | US-11-313-450-25 | Sequence 25, Appl |
| 1116 | 61 | 5.1 | 911 | 7 | US-11-449-902-41149 | Sequence 41149, A |
| 1117 | 61 | 5.1 | 1079 | 7 | US-11-449-902-53619 | Sequence 53619, A |
| 1118 | 61 | 5.1 | 1279 | 7 | US-11-056-355B-80755 | Sequence 80755, A |
| 1119 | 61 | 5.1 | 1432 | 7 | US-11-056-355B-80754 | Sequence 80754, A |
| 1120 | 61 | 5.1 | 1458 | 7 | US-11-056-355B-84133 | Sequence 84133, A |
| 1121 | 61 | 5.1 | 1471 | 7 | US-11-056-355B-84132 | Sequence 84132, A |
| 1122 | 61 | 5.1 | 1487 | 7 | US-11-056-355B-84132 | Sequence 84132, A |
| 1123 | 61 | 5.1 | 1487 | 7 | US-11-056-355B-84131 | Sequence 84131, A |
| 1124 | 61 | 5.1 | 1493 | 7 | US-11-056-355B-84131 | Sequence 84131, A |

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| 1125 | 61 | 5.1 | 1503 | 7 | US-11-312-958-48 | Sequence 48, Appl |
| 1126 | 61 | 5.1 | 1913 | 7 | US-11-063-439-163 | Sequence 163, App |
| 1127 | 61 | 5.1 | 1954 | 7 | US-11-090-997-1036 | Sequence 1036, Ap |
| 1128 | 61 | 5.1 | 1963 | 7 | US-11-090-997-1038 | Sequence 1038, Ap |
| 1129 | 61 | 5.1 | 2530 | 7 | US-11-046-560A-23 | Sequence 23, Appl |
| 1130 | 61 | 5.1 | 3011 | 6 | US-10-520-153-14 | Sequence 14, Appl |
| 1131 | 61 | 5.1 | 3011 | 6 | US-10-527-422-16 | Sequence 16, Appl |
| 1132 | 61 | 5.1 | 3011 | 7 | US-11-140-487A-771 | Sequence 771, Appl |
| 1133 | 61 | 5.1 | 3011 | 7 | US-11-236-835-14 | Sequence 14, Appl |
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| 1135 | 61 | 5.1 | 3011 | 7 | US-11-411-493-1 | Sequence 1, Appli |
| 1136 | 61 | 5.1 | 3011 | 7 | US-11-397-236A-3 | Sequence 3, Appli |
| 1137 | 61 | 5.1 | 3203 | 7 | US-11-063-439-171 | Sequence 171, App |
| 1138 | 61 | 5.1 | 3222 | 7 | US-11-063-439-137 | Sequence 137, App |
| 1139 | 61 | 5.1 | 3469 | 7 | US-11-063-439-106 | Sequence 106, App |
| 1140 | 61 | 5.1 | 3473 | 7 | US-11-063-439-126 | Sequence 126, App |
| 1141 | 61 | 5.1 | 3490 | 7 | US-11-063-439-173 | Sequence 173, App |
| 1142 | 61 | 5.1 | 3496 | 7 | US-11-063-439-172 | Sequence 172, App |
| 1143 | 61 | 5.1 | 3497 | 7 | US-11-063-439-116 | Sequence 116, App |
| 1144 | 61 | 5.1 | 3499 | 7 | US-11-063-439-196 | Sequence 196, App |
| 1145 | 61 | 5.1 | 3507 | 7 | US-11-063-439-166 | Sequence 166, App |
| 1146 | 61 | 5.1 | 3508 | 7 | US-11-063-439-168 | Sequence 168, App |
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| 1148 | 60.5 | 5.1 | 172 | 6 | US-10-090-997-56705 | Sequence 56705, A |
| 1149 | 60.5 | 5.1 | 146 | 6 | US-10-953-349-23775 | Sequence 23775, A |
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| 1153 | 60.5 | 5.1 | 270 | 7 | US-11-133-075-63 | Sequence 63, Appl |
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| 1156 | 60.5 | 5.1 | 283 | 7 | US-11-056-355B-9775 | Sequence 9775, A |
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| 1163 | 60.5 | 5.1 | 324 | 7 | US-11-056-355B-26769 | Sequence 26769, A |
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| 1166 | 60.5 | 5.1 | 367 | 6 | US-11-452-213-10 | Sequence 10, Appl |
| 1167 | 60.5 | 5.1 | 374 | 6 | US-10-449-902-29574 | Sequence 29574, A |
| 1168 | 60.5 | 5.1 | 376 | 7 | US-11-056-355B-26767 | Sequence 26767, A |
| 1169 | 60.5 | 5.1 | 376 | 7 | US-11-056-355B-48003 | Sequence 48003, A |
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| 1171 | 60.5 | 5.1 | 405 | 7 | US-11-056-355B-108131 | Sequence 108131, |
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| 1174 | 60.5 | 5.1 | 405 | 7 | US-11-434-199-2214 | Sequence 2214, Ap |
| 1175 | 60.5 | 5.1 | 413 | 7 | US-11-434-203-2214 | Sequence 2214, Ap |
| 1176 | 60.5 | 5.1 | 423 | 7 | US-11-434-184-2214 | Sequence 2214, Ap |
| 1177 | 60.5 | 5.1 | 423 | 7 | US-11-056-355B-846 | Sequence 846, App |
| 1178 | 60.5 | 5.1 | 443 | 6 | US-11-056-355B-108129 | Sequence 108129, |
| 1179 | 60.5 | 5.1 | 443 | 7 | US-11-056-355B-119368 | Sequence 119368, |
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| 1183 | 60.5 | 5.1 | 460 | 7 | US-11-330-403-18920 | Sequence 18920, A |
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| 1185 | 60.5 | 5.1 | 464 | 7 | US-11-056-355B-65841 | Sequence 65841, A |
| 1186 | 60.5 | 5.1 | 472 | 6 | US-11-471-571A-4034 | Sequence 4034, Ap |
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| 1188 | 60.5 | 5.1 | 491 | 7 | US-11-056-355B-80145 | Sequence 80145, A |
| 1189 | 60.5 | 5.1 | 493 | 7 | US-11-315-766-29 | Sequence 29, Appl |
| 1190 | 60.5 | 5.1 | 512 | 7 | US-11-056-355B-65840 | Sequence 65840, A |
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| 1192 | 60.5 | 5.1 | 519 | 7 | US-11-056-355B-20240 | Sequence 20240, A |
| 1193 | 60.5 | 5.1 | 586 | 7 | US-11-056-355B-65833 | Sequence 65833, A |
| 1194 | 60.5 | 5.1 | 619 | 6 | US-11-056-355B-56241 | Sequence 56241, A |
| 1195 | 60.5 | 5.1 | 625 | 6 | US-11-330-403-11192 | Sequence 11192, A |
| 1196 | 60.5 | 5.1 | 629 | 6 | US-10-953-349-31706 | Sequence 31706, A |
| 1197 | 60.5 | 5.1 | 629 | 7 | US-10-056-355B-66693 | Sequence 66693, A |
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| 1213 | 60.5 | 5.1 | 795 | 6 | US-10-449-902-44893 | Sequence 44893, A |
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| 1219 | 60.5 | 5.1 | 3466 | 7 | US-11-063-439-169 | Sequence 169, App |
| 1220 | 60.5 | 5.1 | 3486 | 7 | US-11-063-439-167 | Sequence 167, App |
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| 1222 | 60.5 | 5.1 | 3495 | 6 | US-11-063-439-123 | Sequence 123, App |
| 1223 | 60.5 | 5.1 | 3496 | 7 | US-11-063-439-186 | Sequence 186, App |
| 1224 | 60.5 | 5.1 | 3502 | 6 | US-11-063-439-136 | Sequence 136, App |
| 1225 | 60.5 | 5.1 | 3509 | 7 | US-11-063-439-176 | Sequence 176, App |
| 1226 | 60.5 | 5.1 | 3509 | 7 | US-11-063-439-178 | Sequence 178, App |
| 1227 | 60.5 | 5.1 | 3511 | 7 | US-11-063-439-224 | Sequence 224, App |
| 1228 | 60.5 | 5.1 | 3511 | 7 | US-11-063-439-72 | Sequence 72, App |
| 1229 | 60.5 | 5.1 | 3512 | 7 | US-11-063-439-122 | Sequence 122, App |
| 1230 | 60.5 | 5.1 | 3512 | 7 | US-11-063-439-191 | Sequence 191, App |
| 1231 | 60.5 | 5.1 | 3516 | 7 | US-11-063-439-161 | Sequence 161, App |
| 1232 | 60.5 | 5.1 | 3518 | 7 | US-11-063-439-154 | Sequence 154, App |
| 1233 | 60.5 | 5.1 | 3518 | 7 | US-11-063-439-187 | Sequence 187, App |
| 1234 | 60.5 | 5.1 | 3519 | 7 | US-11-063-439-189 | Sequence 189, App |
| 1235 | 60.5 | 5.1 | 3519 | 7 | US-11-063-439-122 | Sequence 122, App |
| 1236 | 60.5 | 5.1 | 3523 | 7 | US-11-063-439-146 | Sequence 146, App |
| 1237 | 60.5 | 5.1 | 3523 | 7 | US-11-063-439-152 | Sequence 152, App |
| 1238 | 60.5 | 5.1 | 3524 | 7 | US-11-063-439-124 | Sequence 124, App |
| 1239 | 60.5 | 5.1 | 3528 | 7 | US-11-063-439-155 | Sequence 155, App |
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| 1241 | 60.5 | 5.1 | 3531 | 7 | US-11-063-439-139 | Sequence 139, App |
| 1242 | 60.5 | 5.1 | 3534 | 7 | US-11-063-439-132 | Sequence 132, App |
| 1243 | 60.5 | 5.1 | 3540 | 7 | US-11-063-439-188 | Sequence 188, App |
| 1244 | 60.5 | 5.1 | 3541 | 7 | US-11-063-439-128 | Sequence 128, App |
| 1245 | 60.5 | 5.1 | 3542 | 7 | US-11-063-439-212 | Sequence 212, App |
| 1246 | 60.5 | 5.1 | 3544 | 7 | US-11-063-439-159 | Sequence 159, App |
| 1247 | 60.5 | 5.1 | 3544 | 7 | US-11-063-439-197 | Sequence 197, App |
| 1248 | 60.5 | 5.1 | 3544 | 7 | US-11-063-439-138 | Sequence 138, App |
| 1249 | 60.5 | 5.1 | 3551 | 7 | US-11-063-439-192 | Sequence 192, App |
| 1250 | 60.5 | 5.1 | 3551 | 7 | US-11-063-439-120 | Sequence 120, App |
| 1251 | 60.5 | 5.1 | 3561 | 7 | US-11-063-439-165 | Sequence 165, App |
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| 1253 | 60.5 | 5.1 | 3573 | 6 | US-11-366-965-394 | Sequence 394, App |
| 1254 | 60 | 5.1 | 87 | 6 | US-11-612-783-6739 | Sequence 6739, App |
| 1255 | 60 | 5.0 | 167 | 7 | US-10-366-965-394 | Sequence 394, App |
| 1256 | 60 | 5.0 | 180 | 7 | US-11-056-355B-66028 | Sequence 66028, A |
| 1257 | 60 | 5.0 | 201 | 7 | US-10-522-341A-12 | Sequence 12, Appl |
| 1258 | 60 | 5.0 | 205 | 6 | US-10-449-902-32555 | Sequence 32555, Ap |
| 1259 | 60 | 5.0 | 205 | 6 | US-10-449-902-42627 | Sequence 42627, A |
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| 1262 | 60 | 5.0 | 247 | 7 | US-10-471-571A-1730 | Sequence 1730, App |
| 1263 | 60 | 5.0 | 258 | 6 | US-11-056-355B-80675 | Sequence 80675, A |
| 1264 | 60 | 5.0 | 258 | 7 | US-10-471-571A-1624 | Sequence 1624, App |
| 1265 | 60 | 5.0 | 263 | 6 | US-10-449-902-43208 | Sequence 43208, Ap |
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| 1267 | 60 | 5.0 | 266 | 6 | US-10-449-902-32147 | Sequence 32147, A |
| 1268 | 60 | 5.0 | 266 | 6 | US-10-449-902-32787 | Sequence 32787, A |
| 1269 | 60 | 5.0 | 266 | 6 | US-10-449-902-54901 | Sequence 54901, A |

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| 1271 | 60 | 5.0 | 275 | 7 | US-11-434-137-846 | Sequence 846, App |
| 1272 | 60 | 5.0 | 275 | 7 | US-11-434-184-846 | Sequence 846, App |
| 1273 | 60 | 5.0 | 275 | 7 | US-11-434-199-846 | Sequence 846, App |
| 1274 | 60 | 5.0 | 275 | 7 | US-11-434-203-846 | Sequence 846, App |
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| 1283 | 60 | 5.0 | 333 | 7 | US-11-404-939-509 | Sequence 509, App |
| 1284 | 60 | 5.0 | 347 | 6 | US-11-571A-5228 | Sequence 5228, App |
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| 1289 | 60 | 5.0 | 367 | 6 | US-11-434-199-6806 | Sequence 6806, Ap |
| 1290 | 60 | 5.0 | 367 | 7 | US-11-434-203-6806 | Sequence 6806, Ap |
| 1291 | 60 | 5.0 | 367 | 7 | US-11-221-332-116 | Sequence 116, App |
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| 1303 | 60 | 5.0 | 463 | 7 | US-11-434-184-900 | Sequence 900, App |
| 1304 | 60 | 5.0 | 463 | 7 | US-11-434-199-900 | Sequence 900, App |
| 1305 | 60 | 5.0 | 463 | 7 | US-11-434-203-900 | Sequence 900, App |
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| 1307 | 60 | 5.0 | 472 | 6 | US-11-056-355B-36420 | Sequence 36420, A |
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| 1310 | 60 | 5.0 | 506 | 7 | US-11-366-965-214 | Sequence 214, App |
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| 1328 | 60 | 5.0 | 792 | 7 | US-11-434-199-10146 | Sequence 10146, A |
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| 1476 | 59 | 4.9 | 189 | 7 | US-11-056-355B-51827 | Sequence 51827, A |
| 1477 | 59 | 4.9 | 194 | 7 | US-11-056-355B-3122 | Sequence 3122, Ap |
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| 1493 | 59 | 4.9 | 289 | 7 | US-11-056-355B-45249 | Sequence 45249, A |
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Job time : 56 secs

QM protein - protein search, using sw model

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Run on: October 31, 2006, 02:24:29 ; Search time 43 Seconds
(without alignments)
523.598 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
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Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : 1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
PIR_80:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 664 | 55.6 | 445 | 2 | I38027 | MLN 64 protein - h |
| 2 | 204 | 17.1 | 478 | 2 | T16170 | hypothetical prote |
| 3 | 102.5 | 8.6 | 348 | 2 | H90281 | hypothetical prote |
| 4 | 93.5 | 7.8 | 424 | 2 | D75080 | glucose-1-phosphat |
| 5 | 90 | 7.5 | 1911 | 2 | T43048 | calcium channel al |
| 6 | 86.5 | 7.2 | 767 | 2 | T21969 | hypothetical prote |
| 7 | 85.5 | 7.2 | 396 | 2 | B81299 | probable molybdopt |
| 8 | 85.5 | 7.2 | 438 | 2 | A57219 | Batten disease-rel |
| 9 | 85 | 7.1 | 448 | 2 | G70172 | conserved hypothet |
| 10 | 84.5 | 7.1 | 471 | 2 | A41680 | integral membrane |
| 11 | 83.5 | 7.0 | 352 | 2 | H97002 | probable integral |
| 12 | 83 | 6.9 | 291 | 2 | AE0302 | sugar ABC transpor |
| 13 | 83 | 6.9 | 590 | 1 | S34960 | NADH2 dehydrogenas |
| 14 | 82.5 | 6.9 | 186 | 2 | B29835 | TraS protein - Esc |
| 15 | 82.5 | 6.9 | 239 | 1 | C64227 | hypothetical prote |
| 16 | 82.5 | 6.9 | 341 | 2 | S51265 | probable N-acetylg |
| 17 | 82.5 | 6.9 | 406 | 2 | T43120 | conserved hypothet |
| 18 | 82.5 | 6.9 | 891 | 2 | T37397 | major core protein |
| 19 | 82 | 6.9 | 589 | 2 | T52070 | RNA1 protein homol |
| 20 | 82 | 6.9 | 589 | 2 | A36983 | RNA1 homolog fug1 |
| 21 | 82 | 6.9 | 1466 | 2 | T30566 | ATP-binding casset |
| 22 | 81 | 6.8 | 385 | 2 | B84447 | hypothetical prote |
| 23 | 81 | 6.8 | 529 | 2 | T23190 | hypothetical prote |
| 24 | 81 | 6.8 | 532 | 2 | S46831 | probable membrane |
| 25 | 80.5 | 6.7 | 156 | 2 | I84498 | melatonin receptor |
| 26 | 80.5 | 6.7 | 322 | 2 | T45568 | hypothetical prote |
| 27 | 80.5 | 6.7 | 396 | 2 | T50229 | probable transmemb |
| 28 | 80.5 | 6.7 | 417 | 2 | C44038 | tryptophan permeas |
| 29 | 80.5 | 6.7 | 463 | 2 | AE1155 | amino acid transpo |
| 30 | 80.5 | 6.7 | 536 | 2 | A71491 | probable integral |
| 31 | 80.5 | 6.7 | 644 | 2 | S63056 | probable membrane |
| 32 | 80.5 | 6.7 | 738 | 2 | S10659 | membrane protein t |
| 33 | 80.5 | 6.7 | 891 | 1 | WMVZ3S | major core protein |
| 34 | 80.5 | 6.7 | 891 | 1 | WMVZ3W | major core protein |
| 35 | 80.5 | 6.7 | 1780 | 2 | A85045 | probable glucan sy |
| 36 | 80 | 6.7 | 103 | 2 | G75513 | conserved hypothet |
| 37 | 80 | 6.7 | 290 | 2 | D89898 | hypothetical membr |
| 38 | 80 | 6.7 | 309 | 2 | EDBEIC | RTM1 protein - yea |
| 39 | 80 | 6.7 | 388 | 2 | S59140 | hypothetical prote |
| 40 | 80 | 6.7 | 891 | 1 | H71115 | probable SNF2 subf |
| 41 | 79.5 | 6.7 | 463 | 2 | AF1532 | spermidine/putresc |
| 42 | 79.5 | 6.7 | 491 | 1 | AH1513 | amino acid transpo |
| 43 | 78.5 | 6.6 | 239 | 2 | S73812 | immediate-early pr |
| 44 | 78.5 | 6.6 | 269 | 2 | AF1532 | spermidine/putresc |
| 45 | 78.5 | 6.6 | 358 | 2 | F64136 | rnfD protein homol |
| 46 | 78.5 | 6.6 | 471 | 1 | S11280 | serotonin receptor |
| 47 | 78 | 6.6 | 678 | 2 | S44925 | IB3/5-polypeptide |
| 48 | 78 | 6.5 | 245 | 2 | JC5346 | cdd2 protein - Clo |
| 49 | 78 | 6.5 | 259 | 2 | F83825 | hypothetical prote |
| 50 | 78 | 6.5 | 382 | 2 | E97157 | stage III sporulat |
| 51 | 77.5 | 6.5 | 471 | 2 | B64099 | undecaprenyl-phosp |
| 52 | 78 | 6.5 | 1297 | 2 | T39287 | hypothetical prote |
| 53 | 77.5 | 6.5 | 2136 | 2 | F83130 | spermidine/putresc |
| 54 | 77.5 | 6.5 | 269 | 2 | A05037 | probable membrane |
| 55 | 77.5 | 6.5 | 299 | 2 | AH1175 | conserved hypothet |
| 56 | 77.5 | 6.5 | 327 | 2 | AE0461 | ABC transporter (p |
| 57 | 77.5 | 6.5 | 328 | 2 | F82904 | hypothetical prote |
| 58 | 77.5 | 6.5 | 338 | 2 | F84130 | hypothetical prote |
| 59 | 77.5 | 6.5 | 440 | 2 | T39159 | NADH2 dehydrogenas |
| 60 | 77.5 | 6.5 | 491 | 2 | T11319 | sodium- and chlori |
| 61 | 77.5 | 6.5 | 512 | 2 | B69499 | probable colanic b |
| 62 | 77.5 | 6.5 | 734 | 1 | AC3399 | NADH2 dehydrogenas |
| 63 | 77.5 | 6.5 | 892 | 2 | DER2N5 | A11L protein - var |
| 64 | 77.5 | 6.5 | 892 | 2 | H72164 | hypothetical prote |
| 65 | 77.5 | 6.5 | 892 | 2 | T28552 | A10I protein - var |
| 66 | 77.5 | 6.5 | 1784 | 2 | B36849 | sodium channel pro |
| 67 | 77 | 6.4 | 332 | 2 | C87307 | hypothetical secre |
| 68 | 77 | 6.4 | 559 | 2 | A90072 | hypothetical trans |
| 69 | 77 | 6.4 | 590 | 1 | QOUTC5 | NADH2 dehydrogenas |
| 70 | 77 | 6.4 | 650 | 1 | QQUTC5 | hypothetical prote |
| 71 | 77 | 6.4 | 991 | 2 | T01377 | NADH2 dehydrogenas |
| 72 | 77 | 6.4 | 1025 | 2 | T18376 | hypothetical prote |
| 73 | 77 | 6.4 | 1117 | 2 | T11476 | hypothetical prote |
| 74 | 77 | 6.4 | 1500 | 2 | T24184 | hypothetical prote |
| 75 | 76.5 | 6.4 | 278 | 2 | T48466 | hypothetical prote |
| 76 | 76.5 | 6.4 | 282 | 2 | T24664 | phage tail fibe |
| 77 | 76.5 | 6.4 | 352 | 2 | JC6139 | probable tail prot |
| 78 | 76.5 | 6.4 | 1450 | 2 | T37258 | probable sugar ABC |
| 79 | 76.5 | 6.4 | 1783 | 2 | C88728 | hypothetical prote |
| 80 | 76 | 6.4 | 1917 | 2 | C88728 | cystic fibrosis tr |
| 81 | 76.5 | 6.4 | 156 | 2 | I62107 | protein C48A7.1 [i |
| 82 | 76.5 | 6.4 | 263 | 2 | G95198 | probable voltage-d |
| 83 | 76.5 | 6.4 | 263 | 2 | C98065 | melatonin receptor |
| 84 | 76 | 6.4 | 342 | 2 | E82211 | hypothetical recep |
| 85 | 76 | 6.3 | 402 | 2 | H64919 | hypothetical prote |
| 86 | 76 | 6.3 | 669 | 2 | B85807 | conserved hypothet |
| 87 | 76 | 6.3 | 402 | 2 | H90958 | hypothetical prote |
| 88 | 76 | 6.3 | 352 | 2 | H95869 | probable membrane |
| 89 | 76 | 6.3 | 339 | 2 | S85769 | hypothetical prote |
| 90 | 76 | 6.3 | 352 | 2 | C90921 | hypothetical prote |
| 91 | 75.5 | 6.3 | 263 | 2 | F91209 | low affinity trypt |
| 92 | 75.5 | 6.3 | 156 | 2 | C90921 | low affinity trypt |
| 93 | 75.5 | 6.3 | 415 | 2 | A86056 | hypothetical prote |
| 94 | 75.5 | 6.3 | 352 | 2 | A39412 | probable membrane |
| 95 | 75.5 | 6.3 | 352 | 2 | A86056 | conserved hypothet |
| 96 | 75.5 | 6.3 | 415 | 2 | C90921 | hypothetical prote |
| 97 | 75.5 | 6.3 | 415 | 2 | S85769 | probable membrane |
| 98 | 75.5 | 6.3 | 415 | 2 | E82211 | hypothetical prote |
| 99 | 75.5 | 6.3 | 415 | 2 | H64919 | hypothetical prote |
| 100 | 75.5 | 6.3 | 471 | 2 | A86056 | tryptophan transpo |
| 101 | 75.5 | 6.3 | 471 | 2 | S40689 | 5-hydroxytryptamin |
| 102 | 75.5 | 6.3 | 498 | 2 | T11039 | NADH2 dehydrogenas |

| No. | Score | pI | Ct | Accession | Description |
|---|---|---|---|---|---|
| 103 | 75.5 | 6.3 | 2 | H64594 | multidrug resistan |
| 104 | 75.5 | 6.3 | 2 | T29669 | hypothetical prote |
| 105 | 75.5 | 6.3 | 2 | T52107 | anion channel prot |
| 106 | 75.5 | 6.3 | 2 | T39103 | probable negative |
| 107 | 75 | 6.3 | 2 | A82509 | sulfate/thiosulfat |
| 108 | 75 | 6.3 | 2 | G64470 | probable phosphati |
| 109 | 75 | 6.3 | 2 | B71163 | probable oligopept |
| 110 | 75 | 6.3 | 2 | A38627 | gamma-aminobutyric |
| 111 | 75 | 6.3 | 2 | T45850 | hypothetical prote |
| 112 | 75 | 6.3 | 2 | C69810 | anion-binding prot |
| 113 | 75 | 6.3 | 2 | H90124 | hypothetical prote |
| 114 | 75 | 6.3 | 1 | D42088 | adenylate cyclase |
| 115 | 74.5 | 6.2 | 1 | A95881 | probable trehalose |
| 116 | 74.5 | 6.2 | 2 | H72420 | oligopeptide ABC t |
| 117 | 74.5 | 6.2 | 2 | JC4304 | orphan G protein-c |
| 118 | 74.5 | 6.2 | 2 | A34863 | serotonin receptor |
| 119 | 74.5 | 6.2 | 2 | B84143 | Na+/H+ antiporter |
| 120 | 74.5 | 6.2 | 2 | T14826 | transcription init |
| 121 | 74.5 | 6.2 | 2 | T05964 | probable low-affin |
| 122 | 74.5 | 6.2 | 2 | S38000 | probable transport |
| 123 | 74.5 | 6.2 | 1 | T47792 | hypothetical prote |
| 124 | 74.5 | 6.2 | 1 | C69540 | cobalamin (5'-phos |
| 125 | 74 | 6.2 | 2 | C86859 | quinone-reactive N |
| 126 | 74 | 6.2 | 2 | B69422 | NADH2 dehydrogenas |
| 127 | 74 | 6.2 | 2 | S26018 | spermidine/putresc |
| 128 | 74 | 6.2 | 2 | S73424 | hypothetical prote |
| 129 | 74 | 6.2 | 2 | C72547 | probable aspartate |
| 130 | 74 | 6.2 | 2 | H86732 | hypothetical prote |
| 131 | 74 | 6.2 | 2 | JC6311 | interferon recepto |
| 132 | 74 | 6.2 | 2 | I38848 | Mel-1a melatonin r |
| 133 | 74 | 6.2 | 2 | H89869 | hypothetical prote |
| 134 | 74 | 6.2 | 2 | C86850 | transmembrane effl |
| 135 | 74 | 6.2 | 2 | S02011 | serotonin receptor |
| 136 | 74 | 6.2 | 2 | T36137 | probable amino aci |
| 137 | 74 | 6.2 | 1 | T24115 | hypothetical prote |
| 138 | 74 | 6.2 | 1 | C71417 | cytochrome P450 dl |
| 139 | 74 | 6.2 | 1 | JC7378 | l-lysine 6-aminotr |
| 140 | 73.5 | 6.2 | 2 | T51517 | telomerase reverse |
| 141 | 73.5 | 6.2 | 2 | E95845 | conserved hypothet |
| 142 | 73.5 | 6.2 | 2 | A84727 | hypothetical prote |
| 143 | 73.5 | 6.2 | 2 | G70474 | hypothetical prote |
| 144 | 73.5 | 6.2 | 2 | S76713 | hypothetical prote |
| 145 | 73.5 | 6.2 | 2 | I40448 | conserved hypothet |
| 146 | 73.5 | 6.2 | 2 | S58448 | ubiquinol-cytochro |
| 147 | 73.5 | 6.2 | 2 | AF0636 | glucans biosynthes |
| 148 | 73.5 | 6.2 | 1 | S01511 | ubiquinol-cytochro |
| 149 | 73.5 | 6.2 | 2 | A69804 | ABC transporter (A |
| 150 | 73.5 | 6.2 | 2 | AD1738 | similar to multidr |
| 151 | 73.5 | 6.2 | 1 | C96672 | hypothetical prote |
| 152 | 73.5 | 6.2 | 2 | EDBEM5 | immediate-early pr |
| 153 | 73.5 | 6.2 | 2 | P82623 | potassium uptake p |
| 154 | 73.5 | 6.2 | 2 | H83945 | DNA mismatch repai |
| 155 | 73.5 | 6.2 | 2 | B32935 | hypothetical prote |
| 156 | 73.5 | 6.2 | 2 | T31914 | hypothetical prote |
| 157 | 73.5 | 6.2 | 2 | E96744 | probable oligopept |
| 158 | 73 | 6.2 | 2 | A39927 | RNA-directed RNA p |
| 159 | 73 | 6.1 | 2 | F71925 | cag island protein |
| 160 | 73 | 6.1 | 2 | S26030 | NADH2 dehydrogenas |
| 161 | 73 | 6.1 | 2 | T15560 | hypothetical prote |
| 162 | 73 | 6.1 | 1 | WZBEE4 | 49.2K membrane pro |
| 163 | 73 | 6.1 | 2 | T30985 | hypothetical prote |
| 164 | 73 | 6.1 | 2 | A71823 | hypothetical prote |
| 165 | 73 | 6.1 | 2 | G89901 | hypothetical prote |
| 166 | 73 | 6.1 | 2 | T00268 | hypothetical prote |
| 167 | 73 | 6.1 | 2 | B96508 | hypothetical prote |
| 168 | 72.5 | 6.1 | 2 | S20901 | titin - rabbit (fr |
| 169 | 72.5 | 6.1 | 2 | S72929 | hypothetical prote |
| 170 | 72.5 | 6.1 | 2 | B85866 | probable transport |
| 171 | 72.5 | 6.1 | 2 | B91022 | probable transport |
| 172 | 72.5 | 6.1 | 2 | H64996 | hypothetical prote |
| 173 | 72.5 | 6.1 | 2 | A60944 | ubiquinol-cytochro |
| 174 | 72.5 | 6.1 | 2 | T02986 | chlorophyll a/b-bi |
| 175 | 72.5 | 6.1 | 2 | H96598 | conserved hypothet |
| 176 | 72.5 | 6.1 | 2 | H86670 | hypothetical prote |
| 177 | 72.5 | 6.1 | 2 | C88951 | protein C38C3.2 (i |
| 178 | 72.5 | 6.1 | 2 | A55493 | oxytocin receptor |
| 179 | 72.5 | 6.1 | 2 | AF0173 | probable paraquat- |
| 180 | 72.5 | 6.1 | 2 | H70453 | virulence factor M |
| 181 | 72.5 | 6.1 | 2 | S47631 | pituitary adenylat |
| 182 | 72.5 | 6.1 | 2 | T29705 | hypothetical prote |
| 183 | 72.5 | 6.1 | 2 | T23465 | hypothetical prote |
| 184 | 72.5 | 6.1 | 2 | S57913 | probable transloca |
| 185 | 72.5 | 6.1 | 1 | C84508 | probable cap-bindi |
| 186 | 72.5 | 6.1 | 2 | T30037 | hypothetical prote |
| 187 | 72 | 6.0 | 2 | T21099 | hypothetical prote |
| 188 | 72 | 6.0 | 2 | AE1156 | probable permease |
| 189 | 72 | 6.0 | 2 | G97199 | probable permease |
| 190 | 72 | 6.0 | 2 | T27805 | ubiquinol-cytochro |
| 191 | 72 | 6.0 | 2 | T11349 | late L1 52K protei |
| 192 | 72 | 6.0 | 1 | T07966 | late L1 52K protei |
| 193 | 72 | 6.0 | 2 | S37854 | glycosyl hydrolase |
| 194 | 72 | 6.0 | 2 | WMAD65 | conserved hypothet |
| 195 | 72 | 6.0 | 2 | T39155 | DNA-directed DNA p |
| 196 | 72 | 6.0 | 2 | D89760 | hypothetical prote |
| 197 | 72 | 6.0 | 2 | T20140 | probable ethylene |
| 198 | 72 | 6.0 | 2 | T18291 | hypothetical prote |
| 199 | 72 | 6.0 | 2 | T15338 | hypothetical prote |
| 200 | 72 | 6.0 | 2 | G96611 | hypothetical prote |
| 201 | 71.5 | 6.0 | 2 | S64587 | patched protein - |
| 202 | 71.5 | 6.0 | 2 | T42660 | trp protein - frui |
| 203 | 71.5 | 6.0 | 1 | T39873 | P-glycoprotein 6 - |
| 204 | 71.5 | 6.0 | 2 | T07966 | cytochrome-c oxida |
| 205 | 71.5 | 6.0 | 2 | S52050 | E1 membrane glycop |
| 206 | 71.5 | 6.0 | 1 | MMIH68 | sensory transducti |
| 207 | 71.5 | 6.0 | 2 | H70975 | prostaglandin E(2) |
| 208 | 71.5 | 6.0 | 2 | AB3516 | flagellar biosynth |
| 209 | 71.5 | 6.0 | 2 | S48689 | EP3-alpha receptor |
| 210 | 71.5 | 6.0 | 2 | S51280 | Mel-1a melatonin r |
| 211 | 71.5 | 6.0 | 2 | I46699 | ubiquinol-cytochro |
| 212 | 71.5 | 6.0 | 1 | T11776 | hypothetical prote |
| 213 | 71.5 | 6.0 | 2 | T38194 | hypothetical prote |
| 214 | 71.5 | 6.0 | 2 | S34043 | isotocin receptor |
| 215 | 71.5 | 6.0 | 2 | S66497 | oxytocin receptor |
| 216 | 71.5 | 6.0 | 2 | AD1340 | maltodextrin ABC-t |
| 217 | 71.5 | 6.0 | 2 | AB1711 | maltodextrin ABC-t |
| 218 | 71.5 | 6.0 | 2 | PS0154 | 125K surface antig |
| 219 | 71.5 | 6.0 | 2 | T10124 | hexose transport p |
| 220 | 71.5 | 6.0 | 2 | T02499 | hypothetical prote |
| 221 | 71.5 | 6.0 | 2 | H90061 | hypothetical prote |
| 222 | 71.5 | 6.0 | 2 | T46050 | betr protein homol |
| 223 | 71.5 | 6.0 | 1 | D64137 | mediates transport |
| 224 | 71.5 | 6.0 | 2 | A49580 | adenylate cyclase |
| 225 | 71.5 | 5.9 | 2 | B42239 | genome polyprotein |
| 226 | 71.5 | 5.9 | 2 | T34472 | cag pathogenicity |
| 227 | 71.5 | 5.9 | 1 | S18030 | E1 membrane glycop |
| 228 | 71.5 | 5.9 | 2 | B42239 | conserved hypothet |
| 229 | 71.5 | 5.9 | 2 | H64586 | probable processin |
| 230 | 71.5 | 5.9 | 1 | MMIHAI | chlorophyll a/b-bi |
| 231 | 71 | 5.9 | 2 | A82367 | hypothetical prote |
| 232 | 71 | 5.9 | 2 | A81355 | NADH2 dehydrogenas |
| 233 | 71 | 5.9 | 2 | S33443 | hypothetical prote |
| 234 | 71 | 5.9 | 2 | S33443 | hypothetical prote |
| 235 | 71 | 5.9 | 2 | T16745 | 3-deoxy-D-manno-oc |
| 236 | 71 | 5.9 | 2 | T12372 | transcription regu |
| 237 | 71 | 5.9 | 2 | T25561 | serotonin receptor |
| 238 | 71 | 5.9 | 2 | C90603 | |
| 239 | 71 | 5.9 | 2 | F86759 | |
| 240 | 71 | 5.9 | 2 | C90603 | |
| 241 | 71 | 5.9 | 2 | T16745 | |
| 242 | 71 | 5.9 | 2 | F87286 | |
| 243 | 71 | 5.9 | 2 | F86759 | |
| 244 | 71 | 5.9 | 2 | F86759 | |
| 245 | 71 | 5.9 | 2 | F87286 | |
| 246 | 71 | 5.9 | 2 | AF1335 | |
| 247 | 71 | 5.9 | 2 | AF1335 | |
| 248 | 71 | 5.9 | 2 | A43956 | |

| No. | | | | | Accession | Description |
|---|---|---|---|---|---|---|
| 249 | 71 | 5.9 | 546 | 2 | S48932 | hypothetical prote |
| 250 | 71 | 5.9 | 563 | 2 | T38766 | probable transcrip |
| 251 | 71 | 5.9 | 576 | 2 | T22509 | probable membrane |
| 252 | 71 | 5.9 | 620 | 2 | A58932 | cytochrome C-type |
| 253 | 71 | 5.9 | 676 | 2 | E96725 | hypothetical prote |
| 254 | 71 | 5.9 | 788 | 2 | E71813 | probable cytochrom |
| 255 | 71 | 5.9 | 913 | 2 | T52485 | neurofilament prot |
| 256 | 71 | 5.9 | 2437 | 2 | T18482 | probable component |
| 257 | 70.5 | 5.9 | 203 | 1 | T31684 | hypothetical prote |
| 258 | 70.5 | 5.9 | 266 | 2 | H98208 | probable bacitraci |
| 259 | 70.5 | 5.9 | 266 | 2 | B90537 | hypothetical prote |
| 260 | 70.5 | 5.9 | 266 | 2 | T41414 | probable permease |
| 261 | 70.5 | 5.9 | 279 | 2 | AH2408 | permease protein o |
| 262 | 70.5 | 5.9 | 291 | 2 | S22041 | probable receptor- |
| 263 | 70.5 | 5.9 | 340 | 2 | S76294 | hypothetical prote |
| 264 | 70.5 | 5.9 | 352 | 2 | B90537 | hypothetical prote |
| 265 | 70.5 | 5.9 | 365 | 2 | I38748 | protaglandin recep |
| 266 | 70.5 | 5.9 | 365 | 2 | S51315 | protaglandin E re |
| 267 | 70.5 | 5.9 | 374 | 2 | I38747 | protaglandin E re |
| 268 | 70.5 | 5.9 | 374 | 2 | S51317 | protaglandin E re |
| 269 | 70.5 | 5.9 | 388 | 2 | S51316 | protaglandin E re |
| 270 | 70.5 | 5.9 | 388 | 2 | I38750 | protaglandin E re |
| 271 | 70.5 | 5.9 | 389 | 2 | S71336 | protaglandin recep |
| 272 | 70.5 | 5.9 | 390 | 2 | S43375 | mesotocin receptor |
| 273 | 70.5 | 5.9 | 393 | 2 | E71065 | protaglandin E re |
| 274 | 70.5 | 5.9 | 423 | 1 | ACRTGT | gamma-aminobutyric |
| 275 | 70.5 | 5.9 | 599 | 2 | S51318 | protaglandin E re |
| 276 | 70.5 | 5.9 | 425 | 2 | S51319 | hypothetical prote |
| 277 | 70.5 | 5.9 | 472 | 2 | AG3600 | cellulose synthase |
| 278 | 70.5 | 5.9 | 496 | 2 | B64638 | chitin synthase (E |
| 279 | 70.5 | 5.9 | 521 | 2 | E64181 | hypothetical prote |
| 280 | 70.5 | 5.9 | 548 | 2 | A81650 | conserved hypothet |
| 281 | 70.5 | 5.9 | 556 | 2 | T16790 | hypothetical prote |
| 282 | 70.5 | 5.9 | 574 | 2 | S45754 | probable membrane |
| 283 | 70.5 | 5.9 | 598 | 2 | F46027 | gamma-aminobutyric |
| 284 | 70.5 | 5.9 | 599 | 1 | ACRTGT | gamma-aminobutyric |
| 285 | 70.5 | 5.9 | 700 | 2 | T10566 | probable serine/th |
| 286 | 70.5 | 5.9 | 766 | 2 | T48463 | hypothetical prote |
| 287 | 70.5 | 5.9 | 1026 | 2 | T18220 | hypothetical prote |
| 288 | 70.5 | 5.9 | 1583 | 2 | F97846 | hypothetical prote |
| 289 | 70.5 | 5.9 | 1787 | 2 | T20160 | hypothetical prote |
| 290 | 70.5 | 5.9 | 5138 | 2 | B96695 | hypothetical prote |
| 291 | 70 | 5.9 | 189 | 2 | T51847 | conserved hypothet |
| 292 | 70 | 5.9 | 199 | 2 | T08902 | manganese-binding |
| 293 | 70 | 5.9 | 213 | 2 | F86310 | protein Flj3.8 [im |
| 294 | 70 | 5.9 | 256 | 2 | T13597 | hypothetical prote |
| 295 | 70 | 5.9 | 287 | 2 | T52317 | hypothetical prote |
| 296 | 70 | 5.9 | 292 | 2 | H64244 | chlorophyll a/b-bi |
| 297 | 70 | 5.9 | 307 | 2 | E95010 | H+-transporting tw |
| 298 | 70 | 5.9 | 307 | 2 | B97882 | ABC transporter, P |
| 299 | 70 | 5.9 | 330 | 2 | T30981 | hypothetical prote |
| 300 | 70 | 5.9 | 333 | 2 | I38974 | G protein-coupled |
| 301 | 70 | 5.9 | 371 | 2 | T46421 | hypothetical prote |
| 302 | 70 | 5.9 | 388 | 2 | A55597 | oxytocin receptor |
| 303 | 70 | 5.9 | 416 | 2 | A85112 | probable ankyrin-r |
| 304 | 70 | 5.9 | 418 | 2 | T08882 | proline/betaine tr |
| 305 | 70 | 5.9 | 420 | 2 | E72357 | sugar ABC transpor |
| 306 | 70 | 5.9 | 427 | 2 | T01905 | hypothetical prote |
| 307 | 70 | 5.9 | 437 | 2 | C91261 | hypothetical prote |
| 308 | 70 | 5.9 | 437 | 2 | G86101 | glutamate-aspartat |
| 309 | 70 | 5.9 | 438 | 2 | AF3215 | glutamate-aspartat |
| 310 | 70 | 5.9 | 450 | 2 | T42595 | ABC transporter, m |
| 311 | 70 | 5.9 | 494 | 2 | B89827 | envelope protein 5 |
| 312 | 70 | 5.9 | 532 | 2 | T49467 | hypothetical prote |
| 313 | 70 | 5.9 | 551 | 2 | A87019 | related to COPi-in |
| 314 | 70 | 5.9 | 554 | 2 | T27878 | hypothetical prote |
| 315 | 70 | 5.9 | 558 | 2 | H72565 | probable cytochrom |
| 316 | 70 | 5.9 | 675 | 2 | T22323 | hypothetical prote |
| 317 | 70 | 5.9 | 735 | 2 | S46830 | urea transport pro |
| 318 | 70 | 5.9 | 963 | 2 | T26022 | hypothetical prote |
| 319 | 70 | 5.9 | 1930 | 1 | F86200 | protein Plx1l.17 |
| 320 | 69.5 | 5.8 | 133 | 1 | MNIHHC | nonstructural prot |
| 321 | 69.5 | 5.8 | 206 | 2 | S76279 | hypothetical prote |

| No. | | | | | Accession | Description |
|---|---|---|---|---|---|---|
| 322 | 69.5 | 5.8 | 285 | 2 | F70194 | hypothetical prote |
| 323 | 69.5 | 5.8 | 321 | 2 | S59388 | probable membrane |
| 324 | 69.5 | 5.8 | 339 | 2 | A97736 | hypothetical prote |
| 325 | 69.5 | 5.8 | 347 | 2 | G90444 | hypothetical prote |
| 326 | 69.5 | 5.8 | 354 | 2 | I58186 | probable G protein |
| 327 | 69.5 | 5.8 | 361 | 2 | A53216 | prostaglandin E2 r |
| 328 | 69.5 | 5.8 | 362 | 2 | S36766 | prostaglandin E re |
| 329 | 69.5 | 5.8 | 384 | 2 | S62758 | ubiquinol-cytochro |
| 330 | 69.5 | 5.8 | 385 | 2 | S36767 | prostaglandin E re |
| 331 | 69.5 | 5.8 | 387 | 2 | T32561 | hypothetical prote |
| 332 | 69.5 | 5.8 | 394 | 2 | AG1208 | cell-division prot |
| 333 | 69.5 | 5.8 | 400 | 2 | S51791 | Drosophila transio |
| 334 | 69.5 | 5.8 | 402 | 2 | E90986 | hypothetical prote |
| 335 | 69.5 | 5.8 | 405 | 2 | H85831 | probable colanic a |
| 336 | 69.5 | 5.8 | 405 | 2 | G64971 | probable colanic a |
| 337 | 69.5 | 5.8 | 405 | 2 | B53216 | Putative colanic a |
| 338 | 69.5 | 5.8 | 411 | 2 | S36764 | prostaglandin E2 r |
| 339 | 69.5 | 5.8 | 417 | 2 | G72300 | conserved hypothet |
| 340 | 69.5 | 5.8 | 421 | 2 | T44832 | probable emulsan r |
| 341 | 69.5 | 5.8 | 436 | 2 | D98003 | conserved hypothet |
| 342 | 69.5 | 5.8 | 453 | 2 | T25798 | hypothetical prote |
| 343 | 69.5 | 5.8 | 477 | 2 | E82740 | C4-dicarboxylate t |
| 344 | 69.5 | 5.8 | 490 | 2 | B86581 | probable transport |
| 345 | 69.5 | 5.8 | 503 | 2 | C86250 | integral membrane |
| 346 | 69.5 | 5.8 | 507 | 2 | T50054 | hypothetical prote |
| 347 | 69.5 | 5.8 | 515 | 2 | E86634 | organic cation tra |
| 348 | 69.5 | 5.8 | 547 | 2 | F72042 | ADP/ATP translocas |
| 349 | 69.5 | 5.8 | 547 | 2 | G86581 | integral membrane |
| 350 | 69.5 | 5.8 | 557 | 2 | JW0089 | integral membrane |
| 351 | 69.5 | 5.8 | 570 | 2 | AC2137 | organic cation tra |
| 352 | 69.5 | 5.8 | 557 | 2 | B96776 | ABC transporter AT |
| 353 | 69.5 | 5.8 | 570 | 2 | D97337 | hypothetical prote |
| 354 | 69.5 | 5.8 | 579 | 2 | AG1412 | mismatch repair pr |
| 355 | 69.5 | 5.8 | 579 | 2 | S11073 | DNA polymerase III |
| 356 | 69.5 | 5.8 | 604 | 2 | AF1788 | DNA polymerase III |
| 357 | 69.5 | 5.8 | 604 | 2 | T31042 | gamma-aminobutyric |
| 358 | 69.5 | 5.8 | 607 | 2 | F84525 | hypothetical prote |
| 359 | 69.5 | 5.8 | 616 | 2 | B84463 | Mutator-like trans |
| 360 | 69.5 | 5.8 | 877 | 2 | S58824 | Mutator-like trans |
| 361 | 69.5 | 5.8 | 881 | 2 | S46633 | probable membrane |
| 362 | 69.5 | 5.8 | 557 | 2 | S71363 | probable membrane |
| 363 | 69 | 5.8 | 1704 | 2 | A59188 | probable ATP-bindi |
| 364 | 69.5 | 5.8 | 1704 | 2 | JT0382 | ATP-binding casset |
| 365 | 69.5 | 5.8 | 2629 | 2 | JT0382 | uncharacterized my |
| 366 | 69.5 | 5.8 | 7829 | 2 | T45569 | apolipoprotein B - |
| 367 | 69 | 5.8 | 169 | 2 | T15789 | apolipoprotein B - |
| 368 | 69.5 | 5.8 | 244 | 2 | H96934 | hypothetical prote |
| 369 | 69 | 5.8 | 195 | 2 | A96998 | hypothetical prote |
| 370 | 69 | 5.8 | 256 | 2 | H96998 | hypothetical prote |
| 371 | 69 | 5.8 | 261 | 2 | C64145 | hypothetical prote |
| 372 | 69 | 5.8 | 273 | 2 | T07481 | CDP-diglyceride sy |
| 373 | 69 | 5.8 | 273 | 2 | F83805 | hypothetical prote |
| 374 | 69 | 5.8 | 289 | 2 | C71707 | hypothetical prote |
| 375 | 69 | 5.8 | 291 | 2 | S72554 | probable sugar upt |
| 376 | 69 | 5.8 | 300 | 2 | D96002 | ubiquinol-cytochro |
| 377 | 69 | 5.8 | 338 | 2 | T32702 | melatonin receptor |
| 378 | 69 | 5.8 | 339 | 2 | B69436 | hypothetical prote |
| 379 | 69 | 5.8 | 345 | 2 | AH1514 | hypothetical prote |
| 380 | 69 | 5.8 | 351 | 2 | AD0273 | hypothetical prote |
| 381 | 69 | 5.8 | 379 | 2 | S58447 | probable integral |
| 382 | 69 | 5.8 | 382 | 2 | AI3175 | hypothetical prote |
| 383 | 69 | 5.8 | 382 | 2 | D71424 | LSU ribosomal prot |
| 384 | 69 | 5.8 | 386 | 2 | I69644 | hypothetical prote |
| 385 | 69 | 5.8 | 388 | 2 | A99979 | glutamate-aspartat |
| 386 | 69 | 5.8 | 436 | 2 | A42384 | transposase -- Bac |
| 387 | 69 | 5.8 | 437 | 2 | T19512 | gamma-aminobutyric |
| 388 | 69 | 5.8 | 443 | 2 | S25821 | hypothetical prote |
| 389 | 69 | 5.8 | 478 | 2 | T33985 | O-antigen polymera |
| 390 | 69 | 5.8 | 478 | 2 | B96804 | NADH2 dehydrogenas |
| 391 | 69 | 5.8 | 508 | 2 | T11116 | glutamate-aspartat |
| 392 | 69 | 5.8 | 523 | 2 | T24675 | hypothetical prote |
| 393 | 69 | 5.8 | 540 | 2 | E70784 | transposase - Baci |
| 394 | 69 | 5.8 | 549 | 2 | A64100 | probable thioredox |

| ID | % | | Len | n | Accession | Description |
|---|---|---|---|---|---|---|
| 395 | 69 | 5.8 | 599 | 2 | G90476 | probable Na+/H+ an |
| 396 | 69 | 5.8 | 600 | 2 | T11889 | NADH2 dehydrogenas |
| 397 | 69 | 5.8 | 637 | 2 | H96592 | probable multispan |
| 398 | 69 | 5.8 | 659 | 2 | D84633 | hypothetical prote |
| 399 | 69 | 5.8 | 791 | 2 | T12455 | probable oxidoredu |
| 400 | 69 | 5.8 | 802 | 2 | JH0595 | potassium channel |
| 401 | 69 | 5.8 | 863 | 2 | H84490 | hypothetical prote |
| 402 | 69 | 5.8 | 933 | 2 | AD3309 | hypothetical membr |
| 403 | 69 | 5.8 | 1058 | 2 | T30580 | P-type ATPase - sl |
| 404 | 69 | 5.8 | 1344 | 2 | T34188 | myb-binding protei |
| 405 | 69 | 5.8 | 1392 | 2 | T01908 | hypothetical prote |
| 406 | 69 | 5.8 | 1515 | 2 | T04204 | hypothetical prote |
| 407 | 69 | 5.8 | 3010 | 1 | A45573 | genome polyprotein |
| 408 | 68.5 | 5.7 | 225 | 2 | AE0371 | probable carboxype |
| 409 | 68.5 | 5.7 | 237 | 2 | T25877 | probable carboxy |
| 410 | 68.5 | 5.7 | 238 | 2 | T04280 | hypothetical prote |
| 411 | 68.5 | 5.7 | 260 | 2 | H75428 | hypothetical prote |
| 412 | 68.5 | 5.7 | 262 | 2 | AG1830 | hypothetical prote |
| 413 | 68.5 | 5.7 | 265 | 2 | AI3428 | O-antigen export s |
| 414 | 68.5 | 5.7 | 285 | 2 | B86835 | maltose ABC transp |
| 415 | 68.5 | 5.7 | 297 | 2 | S74335 | carbon dioxide con |
| 416 | 68.5 | 5.7 | 304 | 2 | AG3035 | hypothetical prote |
| 417 | 68.5 | 5.7 | 304 | 2 | D98250 | probable sugar ABC |
| 418 | 68.5 | 5.7 | 343 | 2 | AC2129 | iron(III) dicitrat |
| 419 | 68.5 | 5.7 | 359 | 2 | B59105 | hypothetical prote |
| 420 | 68.5 | 5.7 | 362 | 2 | D72424 | oligopeptide ABC t |
| 421 | 68.5 | 5.7 | 377 | 1 | S15308 | omega-3 fatty acid |
| 422 | 68.5 | 5.7 | 383 | 2 | JQ2337 | Edg-1 orphan recep |
| 423 | 68.5 | 5.7 | 391 | 2 | I53870 | probable transmemb |
| 424 | 68.5 | 5.7 | 395 | 2 | H81265 | hypothetical prote |
| 425 | 68.5 | 5.7 | 395 | 2 | B83774 | conserved hypothet |
| 426 | 68.5 | 5.7 | 395 | 2 | A96189 | multidrug resistan |
| 427 | 68.5 | 5.7 | 419 | 2 | AH3097 | Mel-1c receptor su |
| 428 | 68.5 | 5.7 | 420 | 2 | AG1660 | hypothetical prote |
| 429 | 68.5 | 5.7 | 425 | 2 | I51666 | probable glycosylt |
| 430 | 68.5 | 5.7 | 430 | 2 | F97108 | hypothetical prote |
| 431 | 68.5 | 5.7 | 431 | 2 | H72247 | preprotein translo |
| 432 | 68.5 | 5.7 | 444 | 2 | A48260 | corticoliberin rec |
| 433 | 68.5 | 5.7 | 445 | 2 | E22845 | hypothetical prote |
| 434 | 68.5 | 5.7 | 479 | 2 | T44326 | hypothetical prote |
| 435 | 68.5 | 5.7 | 480 | 2 | B70446 | hypothetical prote |
| 436 | 68.5 | 5.7 | 488 | 2 | T15941 | NADH2 dehydrogenas |
| 437 | 68.5 | 5.7 | 492 | 2 | G90574 | hypothetical.prote |
| 438 | 68.5 | 5.7 | 502 | 2 | S77331 | probable cytochrom |
| 439 | 68.5 | 5.7 | 512 | 2 | T00605 | PAC2 protein - yea |
| 440 | 68.5 | 5.7 | 518 | 2 | S50465 | pituitary adenylat |
| 441 | 68.5 | 5.7 | 525 | 2 | JN0902 | hypothetical prote |
| 442 | 68.5 | 5.7 | 542 | 2 | S58102 | Na+ ATPase chain J |
| 443 | 68.5 | 5.7 | 558 | 2 | F64235 | probable ABC trans |
| 444 | 68.5 | 5.7 | 634 | 2 | C83530 | potassium uptake p |
| 445 | 68.5 | 5.7 | 670 | 2 | G86702 | unknown protein [i |
| 446 | 68.5 | 5.7 | 724 | 2 | H86427 | potassium uptake p |
| 447 | 68.5 | 5.7 | 788 | 2 | G64707 | cation-transportin |
| 448 | 68.5 | 5.7 | 923 | 1 | MMBY7C | probable membrane |
| 449 | 68.5 | 5.7 | 1004 | 2 | S55353 | probable copper-tr |
| 450 | 68.5 | 5.7 | 146 | 2 | H75201 | hypothetical prote |
| 451 | 68.5 | 5.7 | 205 | 2 | A64373 | hypothetical prote |
| 452 | 68.5 | 5.7 | 255 | 2 | F39925 | hypothetical prote |
| 453 | 68.5 | 5.7 | 266 | 2 | C95316 | maltose transport |
| 454 | 68.5 | 5.7 | 270 | 2 | AE3627 | bicarbonate transp |
| 455 | 68.5 | 5.7 | 279 | 2 | AG2165 | G protein-coupled |
| 456 | 68.5 | 5.7 | 294 | 2 | T41953 | ribonuclease BN (E |
| 457 | 68.5 | 5.7 | 294 | 2 | AE0004 | COI intron 9 re |
| 458 | 68.5 | 5.7 | 313 | 2 | B38888 | chemokine (C-C) re |
| 459 | 68.5 | 5.7 | 355 | 2 | A45177 | ubiquinol-cytochro |
| 460 | 68.5 | 5.7 | 360 | 2 | T11067 | prostaglandin E re |
| 461 | 68.5 | 5.7 | 364 | 2 | JC2115 | prostaglandin E2 r |
| 462 | 68.5 | 5.7 | 365 | 2 | JC2115 | hypothetical prote |
| 463 | 68.5 | 5.7 | 370 | 2 | H90559 | hypothetical prote |
| 464 | 68.5 | 5.7 | 379 | 2 | H90693 | probable multidrug |
| 465 | 68.5 | 5.7 | 393 | 2 | AG0184 | ubiquinol-cytochro |
| 466 | 68.5 | 5.7 | 402 | 2 | T41253 | hypothetical wfS p |
| 467 | 68 | 5.7 | 417 | 2 | T11387 | NADH2 dehydrogenas |
| 468 | 68 | 5.7 | 426 | 2 | C69831 | conserved hypothet |
| 469 | 68 | 5.7 | 464 | 2 | C70414 | NADH2 dehydrogenas |
| 470 | 68 | 5.7 | 473 | 2 | H71044 | NADH2 dehydrogenas |
| 471 | 68 | 5.7 | 475 | 2 | E83450 | hypothetical prote |
| 472 | 68 | 5.7 | 477 | 2 | H91123 | cytochrome-c oxida |
| 473 | 68 | 5.7 | 477 | 2 | G85968 | probable oxidoredu |
| 474 | 68 | 5.7 | 477 | 2 | C65096 | probable oxidoredu |
| 475 | 68 | 5.7 | 519 | 2 | A35572 | hypothetical prote |
| 476 | 68 | 5.7 | 502 | 1 | I30010 | hypothetical 52.1 |
| 477 | 68 | 5.7 | 519 | 2 | T39918 | prostaglandin E2 r |
| 478 | 68 | 5.7 | 542 | 2 | A69261 | prostaglandin E2 r |
| 479 | 68 | 5.7 | 542 | 2 | B81910 | NADH2 dehydrogenas |
| 480 | 68 | 5.7 | 542 | 2 | B81105 | probable acetyl-co |
| 481 | 68 | 5.7 | 620 | 2 | T19907 | probable acid-CoA |
| 482 | 68 | 5.7 | 664 | 2 | C84869 | probable ABC-trans |
| 483 | 68 | 5.7 | 718 | 2 | E83718 | ABC transporter, A |
| 484 | 68 | 5.7 | 804 | 2 | T49975 | hypothetical prote |
| 485 | 68 | 5.7 | 836 | 2 | T18460 | probable receptor |
| 486 | 68 | 5.7 | 859 | 2 | S69700 | conserved hypothet |
| 487 | 68 | 5.7 | 871 | 2 | H72597 | hypothetical prote |
| 488 | 68 | 5.7 | 1429 | 2 | T19422 | hypothetical prote |
| 489 | 68 | 5.7 | 1878 | 2 | B86189 | conserved hypothet |
| 490 | 68 | 5.7 | 3010 | 1 | GNMVTC | genome polyprotein |
| 491 | 67.5 | 5.6 | 104 | 2 | T36801 | hypothetical prote |
| 492 | 67.5 | 5.6 | 200 | 2 | H72295 | hypothetical prote |
| 493 | 67.5 | 5.6 | 273 | 2 | A97700 | conserved hypothet |
| 494 | 67.5 | 5.6 | 288 | 2 | F72219 | hypothetical prote |
| 495 | 67.5 | 5.6 | 320 | 2 | T23674 | conserved hypothet |
| 496 | 67.5 | 5.6 | 323 | 1 | Q0BEID | HHRF3 protein - hu |
| 497 | 67.5 | 5.6 | 348 | 2 | T12591 | HHRF3 protein - hu |
| 498 | 67.5 | 5.6 | 354 | 2 | T09353 | NADH2 dehydrogenas |
| 499 | 67.5 | 5.6 | 387 | 2 | T24581 | NADH2 dehydrogenas |
| 500 | 67.5 | 5.6 | 387 | 2 | T08086 | G protein-coupled |
| 501 | 67.5 | 5.6 | 397 | 2 | A83999 | protein TI1F1.[i |
| 502 | 67.5 | 5.6 | 419 | 2 | AH1288 | protein TI1F1.[i |
| 503 | 67.5 | 5.6 | 439 | 2 | H83699 | hypothetical prote |
| 504 | 67.5 | 5.6 | 450 | 2 | G91219 | mutants block spor |
| 505 | 67.5 | 5.6 | 450 | 2 | A86066 | multidrug resistan |
| 506 | 67.5 | 5.6 | 450 | 2 | F65183 | sodium-dependent c |
| 507 | 67.5 | 5.6 | 452 | 2 | G89870 | sodium-dependent c |
| 508 | 67.5 | 5.6 | 459 | 2 | JH0594 | TDP-Fuc4NAc lipid |
| 509 | 67.5 | 5.6 | 483 | 2 | G84113 | TDP-Fuc4NAc lipid |
| 510 | 67.5 | 5.6 | 488 | 1 | QXASM4 | 4-alpha-1-fucosylt |
| 511 | 67.5 | 5.6 | 492 | 2 | F64464 | hypothetical prote |
| 512 | 67.5 | 5.6 | 498 | 2 | T48262 | vasoactive intesti |
| 513 | 67.5 | 5.6 | 515 | 2 | H82973 | hypothetical prote |
| 514 | 67.5 | 5.6 | 516 | 2 | H82089 | NADH2 dehydrogenas |
| 515 | 67.5 | 5.6 | 598 | 2 | I51368 | sodium-dependent n |
| 516 | 67.5 | 5.6 | 632 | 1 | A77700 | hypothetical prote |
| 517 | 67.5 | 5.6 | 676 | 2 | T37345 | hypothetical prote |
| 518 | 67.5 | 5.6 | 676 | 2 | D42511 | sensor histidine k |
| 519 | 67.5 | 5.6 | 676 | 2 | F36843 | L8R protein - vari |
| 520 | 67.5 | 5.6 | 676 | 2 | T28500 | hypothetical prote |
| 521 | 67.5 | 5.6 | 676 | 2 | D72158 | ATP/GTP-binding pr |
| 522 | 67.5 | 5.6 | 682 | 2 | G82448 | NPH-II, helicase - |
| 523 | 67.5 | 5.6 | 686 | 2 | S30687 | I8 protein - vacci |
| 524 | 67.5 | 5.6 | 716 | 2 | T02567 | probable dicarboxy |
| 525 | 67.5 | 5.6 | 740 | 1 | I51259 | gamma-aminobutyric |
| 526 | 67.5 | 5.6 | 838 | 2 | A54163 | choline transporte |
| 527 | 67.5 | 5.6 | 866 | 2 | T20574 | hypothetical prote |
| 528 | 67.5 | 5.6 | 866 | 2 | T15915 | probable ATP-bindi |
| 529 | 67.5 | 5.6 | 950 | 2 | T02866 | vacuolar ATPase (E |
| 530 | 67.5 | 5.6 | 1159 | 2 | T19615 | hypothetical prote |
| 531 | 67.5 | 5.6 | 1244 | 2 | S48442 | hypothetical prote |
| 532 | 67.5 | 5.6 | 1411 | 2 | S30855 | ribonuclease - ye |
| 533 | 67.5 | 5.6 | 1753 | 1 | WZV218 | PDR11 protein - ye |
| 534 | 67.5 | 5.6 | 2332 | 2 | GNNYF | hypothetical prote |
| 535 | 67 | 5.6 | 151 | 2 | A72093 | genome polyprotein |
| 536 | 67 | 5.6 | 151 | 2 | H86529 | conserved hypothet |
| 537 | 67 | 5.6 | 159 | 2 | S61040 | CT101 hypothetical |
| 538 | 67 | 5.6 | 159 | 1 | I48129 | probable membrane |
| 539 | 67 | 5.6 | 180 | 2 | D70150 | Xe169 (escapes X-i |
| 540 | 67 | 5.6 | 225 | 1 | D70150 | probable membrane |
| | 67 | 5.6 | 225 | 1 | MMIHIB | E1 membrane glycop |
| | 67 | 5.6 | 244 | 2 | D70404 | conserved hypothet |

| SEQ | | | Len | | Code | Description |
|---|---|---|---|---|---|---|
| 541 | 67 | 5.6 | 255 | 2 | C90078 | hypothetical prote |
| 542 | 67 | 5.6 | 275 | 2 | G98194 | sugar ABC transpor |
| 543 | 67 | 5.6 | 275 | 2 | AC3092 | hypothetical prote |
| 544 | 67 | 5.6 | 275 | 2 | S75698 | hypothetical prote |
| 545 | 67 | 5.6 | 276 | 2 | F69307 | conserved hypothet |
| 546 | 67 | 5.6 | 276 | 2 | S35270 | conserved hypothet |
| 547 | 67 | 5.6 | 283 | 2 | F96959 | DNA-damage repair |
| 548 | 67 | 5.6 | 285 | 2 | AE3024 | tRNA-processing ri |
| 549 | 67 | 5.6 | 286 | 2 | D64235 | hypothetical prote |
| 550 | 67 | 5.6 | 314 | 2 | D96703 | hypothetical prote |
| 551 | 67 | 5.6 | 317 | 2 | D98260 | inner membrane pro |
| 552 | 67 | 5.6 | 336 | 2 | A96997 | ferrichrome transp |
| 553 | 67 | 5.6 | 345 | 2 | T21776 | hypothetical prote |
| 554 | 67 | 5.6 | 349 | 2 | D84166 | hypothetical prote |
| 555 | 67 | 5.6 | 350 | 2 | C88987 | protein C50H11.2 [ |
| 556 | 67 | 5.6 | 352 | 2 | T32314 | hypothetical prote |
| 557 | 67 | 5.6 | 379 | 2 | S58451 | hypothetical prote |
| 558 | 67 | 5.6 | 379 | 2 | S58449 | ubiquinol-cytochro |
| 559 | 67 | 5.6 | 396 | 1 | C69291 | ubiquinol-cytochro |
| 560 | 67 | 5.6 | 407 | 2 | E70309 | pheromone shutdown |
| 561 | 67 | 5.6 | 411 | 2 | B71500 | hypothetical prote |
| 562 | 67 | 5.6 | 415 | 2 | S74041 | glucose transporte |
| 563 | 67 | 5.6 | 416 | 2 | T46401 | glycine betaine tr |
| 564 | 67 | 5.6 | 423 | 2 | C95085 | probable amino aci |
| 565 | 67 | 5.6 | 436 | 2 | AC1021 | pyruvate synthase |
| 566 | 67 | 5.6 | 441 | 2 | F86279 | probable membrane |
| 567 | 67 | 5.6 | 446 | 2 | G72287 | proton glutamate s |
| 568 | 67 | 5.6 | 496 | 2 | A31986 | hypothetical prote |
| 569 | 67 | 5.6 | 507 | 2 | AB1707 | glucose transporte |
| 570 | 67 | 5.6 | 516 | 2 | AE0665 | glycine betaine tr |
| 571 | 67 | 5.6 | 646 | 2 | JC7777 | probable serine/th |
| 572 | 67 | 5.6 | 717 | 2 | T49238 | ATP binding casset |
| 573 | 67 | 5.6 | 753 | 2 | S58331 | hypothetical prote |
| 574 | 67 | 5.6 | 769 | 2 | P81415 | dolichyl-phosphate |
| 575 | 67 | 5.6 | 784 | 2 | C82679 | DNA topoisomerase |
| 576 | 67 | 5.6 | 787 | 2 | PN0677 | cell division prot |
| 577 | 67 | 5.6 | 798 | 2 | T34248 | hypothetical prote |
| 578 | 67 | 5.6 | 814 | 2 | T05537 | probable integral |
| 579 | 67 | 5.6 | 823 | 2 | T35280 | conserved hypothet |
| 580 | 67 | 5.6 | 880 | 2 | D69427 | probable NADH dehy |
| 581 | 67 | 5.6 | 891 | 2 | B82495 | chitin synthase (E |
| 582 | 67 | 5.6 | 900 | 2 | E69631 | galactosamine-cont |
| 583 | 67 | 5.6 | 1175 | 1 | S39951 | DNA-directed DNA p |
| 584 | 67 | 5.6 | 1242 | 1 | DJBEC1 | probable membrane |
| 585 | 67 | 5.6 | 1333 | 2 | S63403 | pleiotropic drug r |
| 586 | 67 | 5.6 | 1511 | 2 | A53151 | conserved hypothet |
| 587 | 67 | 5.6 | 1575 | 2 | G82905 | hypothetical prote |
| 588 | 67 | 5.6 | 1879 | 2 | I19481 | hypothetical prote |
| 589 | 67 | 5.6 | 1905 | 2 | T18267 | sodium channel SCA |
| 590 | 67 | 5.6 | 1993 | 2 | T30902 | genome polyprotein |
| 591 | 67 | 5.6 | 3010 | 1 | GNMVCJ | conserved hypothet |
| 592 | 66.5 | 5.6 | 153 | 2 | G69847 | conserved hypothet |
| 593 | 66.5 | 5.6 | 203 | 2 | T28732 | sugar ABC transpor |
| 594 | 66.5 | 5.6 | 204 | 2 | S70876 | hypothetical prote |
| 595 | 66.5 | 5.6 | 218 | 2 | S77103 | ABC transporter, P |
| 596 | 66.5 | 5.6 | 245 | 2 | A81405 | hypothetical prote |
| 597 | 66.5 | 5.6 | 263 | 2 | AI2384 | cag pathogenicity |
| 598 | 66.5 | 5.6 | 268 | 2 | A70417 | sec-independant pr |
| 599 | 66.5 | 5.6 | 272 | 1 | AI0075 | hypothetical prote |
| 600 | 67 | 5.6 | 279 | 2 | S56642 | hypothetical prote |
| 601 | 66.5 | 5.6 | 279 | 2 | E70322 | nitrate transport |
| 602 | 66.5 | 5.6 | 293 | 2 | A84110 | hypothetical prote |
| 603 | 66.5 | 5.6 | 294 | 2 | S70876 | hypothetical prote |
| 604 | 66.5 | 5.6 | 316 | 2 | C70506 | ABC transporter, P |
| 605 | 66.5 | 5.6 | 333 | 2 | C64586 | hypothetical prote |
| 606 | 66.5 | 5.6 | 347 | 2 | A81405 | hypothetical prote |
| 607 | 66.5 | 5.6 | 356 | 2 | T20737 | hypothetical prote |
| 608 | 66.5 | 5.6 | 359 | 2 | P90055 | conserved hypothet |
| 609 | 66.5 | 5.6 | 367 | 2 | S75836 | hypothetical prote |
| 610 | 66.5 | 5.6 | 380 | 2 | G89786 | hypothetical prote |
| 611 | 66.5 | 5.6 | 384 | 1 | I38890 | hypothetical prote |
| 612 | 66.5 | 5.6 | 389 | 2 | E96516 | F16N3.13 [imported |
| 613 | 66.5 | 5.6 | 400 | 2 | G00013 | D3 dopamine recept |
| 614 | 66.5 | 5.6 | 412 | 2 | G89773 | hypothetical prote |
| 615 | 66.5 | 5.6 | 413 | 2 | H95041 | polysaccharide tra |
| 616 | 66.5 | 5.6 | 435 | 2 | D98111 | hypothetical prote |
| 617 | 66.5 | 5.6 | 435 | 2 | G92246 | maltodextrin ABC t |
| 618 | 66.5 | 5.6 | 453 | 2 | G95135 | MATE efflux family |
| 619 | 66.5 | 5.6 | 462 | 2 | H71228 | hypothetical prote |
| 620 | 66.5 | 5.6 | 488 | 2 | G71969 | cytochrome-c oxida |
| 621 | 66.5 | 5.6 | 490 | 2 | D84998 | cytochrome c-type |
| 622 | 66.5 | 5.6 | 490 | 2 | A63391 | low-affinity inorg |
| 623 | 66.5 | 5.6 | 491 | 2 | AC1555 | cAMP receptor subt |
| 624 | 66.5 | 5.6 | 493 | 2 | A71875 | efflux transporter |
| 625 | 66.5 | 5.6 | 494 | 2 | T32644 | hypothetical prote |
| 626 | 66.5 | 5.6 | 507 | 2 | T27627 | nickel transport s |
| 627 | 66.5 | 5.6 | 539 | 2 | G83720 | hypothetical prote |
| 628 | 66.5 | 5.6 | 547 | 2 | E91135 | probable alkaline |
| 629 | 66.5 | 5.6 | 550 | 1 | H85980 | probable alkaline |
| 630 | 66.5 | 5.6 | 582 | 2 | C71424 | sterol O-acyltrans |
| 631 | 66.5 | 5.6 | 583 | 2 | A11510 | hypothetical prote |
| 632 | 66.5 | 5.6 | 598 | 2 | T32430 | C-terminal domain |
| 633 | 66.5 | 5.6 | 663 | 2 | AG2696 | hypothetical prote |
| 634 | 66.5 | 5.6 | 663 | 2 | G97478 | cytochrome c-type |
| 635 | 66.5 | 5.6 | 727 | 2 | I56506 | cytochrome c-type |
| 636 | 66.5 | 5.6 | 727 | 2 | S27043 | Na+/Cl(-)-dependen |
| 637 | 66.5 | 5.6 | 782 | 2 | S19876 | neurotransmitter t |
| 638 | 66.5 | 5.6 | 889 | 2 | B36786 | genome polyprotein |
| 639 | 66.5 | 5.6 | 992 | 2 | T47311 | hypothetical prote |
| 640 | 66.5 | 5.6 | 992 | 2 | T27479 | hypothetical prote |
| 641 | 66.5 | 5.6 | 1014 | 2 | T31433 | hypothetical prote |
| 642 | 66.5 | 5.6 | 1083 | 2 | C88854 | Na+/Ca2+,K+-exchan |
| 643 | 66.5 | 5.6 | 1083 | 2 | H81037 | protein F11A10.3 [ |
| 644 | 66.5 | 5.6 | 1144 | 2 | T15961 | DNA polymerase III |
| 645 | 66.5 | 5.6 | 1456 | 2 | T15961 | hypothetical prote |
| 646 | 66.5 | 5.6 | 1684 | 2 | JW0057 | gravin - human |
| 647 | 66.5 | 5.6 | 1768 | 2 | B85062 | hypothetical prote |
| 648 | 66.5 | 5.6 | 2151 | 1 | S16449 | hypothetical prote |
| 649 | 66.5 | 5.6 | 2285 | 2 | G02434 | genome polyprotein |
| 650 | 66.5 | 5.6 | 2833 | 2 | A43360 | genome polyprotein |
| 651 | 66.5 | 5.6 | 3011 | 1 | GNWVC3 | DNA-directed DNA p |
| 652 | 66.5 | 5.6 | 93 | 2 | S28759 | inositol 1,4,5-tri |
| 653 | 66.5 | 5.6 | 130 | 1 | D83820 | diacylglycerol kin |
| 654 | 66 | 5.6 | 209 | 2 | A89801 | conserved hypothet |
| 655 | 66 | 5.6 | 276 | 2 | H96816 | hypothetical prote |
| 656 | 66 | 5.6 | 279 | 2 | S42125 | NADH2 dehydrogenas |
| 657 | 66 | 5.6 | 285 | 2 | D87447 | hypothetical prote |
| 658 | 66 | 5.6 | 302 | 2 | A99074 | sulfate ABC transp |
| 659 | 66 | 5.6 | 305 | 2 | I47040 | sterol O-acyltrans |
| 660 | 66 | 5.6 | 317 | 1 | B41671 | hypothetical prote |
| 661 | 66 | 5.6 | 318 | 2 | B84291 | iron transport pro |
| 662 | 66 | 5.6 | 322 | 2 | B71137 | hypothetical prote |
| 663 | 66 | 5.6 | 332 | 2 | C97272 | hypothetical prote |
| 664 | 66 | 5.6 | 370 | 1 | I52315 | conserved membrane |
| 665 | 66 | 5.6 | 379 | 1 | S17405 | G protein-coupled |
| 666 | 66 | 5.6 | 379 | 1 | S17409 | ubiquinol-cytochro |
| 667 | 66 | 5.6 | 379 | 2 | S58460 | ubiquinol-cytochro |
| 668 | 66 | 5.6 | 381 | 2 | A35300 | G protein-coupled |
| 669 | 66 | 5.6 | 390 | 1 | QOBET9 | protein Ut33 - hum |
| 670 | 66 | 5.6 | 397 | 2 | T21154 | hypothetical prote |
| 671 | 66 | 5.6 | 397 | 2 | T44477 | hypothetical prote |
| 672 | 66 | 5.5 | 401 | 2 | B70505 | probable emulsan r |
| 673 | 66 | 5.5 | 401 | 1 | T44831 | probable sugar tra |
| 674 | 66 | 5.5 | 404 | 1 | B64927 | probable sugar tra |
| 675 | 66 | 5.5 | 404 | 2 | A85777 | probable transport |
| 676 | 66 | 5.5 | 404 | 2 | E90928 | probable transport |
| 677 | 66 | 5.5 | 411 | 2 | H86539 | CBS domain protein |
| 678 | 66 | 5.5 | 412 | 2 | A82444 | GGDEF family prote |
| 679 | 66 | 5.5 | 418 | 2 | T41027 | G protein-coupled |
| 680 | 66 | 5.5 | 418 | 2 | B72353 | hypothetical prote |
| 681 | 66 | 5.5 | 424 | 2 | T07366 | hypothetical prote |
| 682 | 66 | 5.5 | 436 | 2 | T14816 | probable phosphati |
| 683 | 66 | 5.5 | 447 | 2 | T18633 | hypothetical prote |
| 684 | 66 | 5.5 | 450 | 2 | A37223 | alpha-2B-adrenergi |
| 685 | 66 | 5.5 | 450 | 2 | A38316 | alpha-2-adrenergic |
| 686 | 66 | 5.5 | 453 | 2 | P86846 | ABC transporter pe |

| No. | % | Val | Len | n | Accession | Description |
|---|---|---|---|---|---|---|
| 687 | 66 | 5.5 | 483 | 2 | S75369 | hypothetical prote |
| 688 | 66 | 5.5 | 484 | 2 | T24238 | hypothetical prote |
| 689 | 66 | 5.5 | 496 | 2 | E82940 | hypothetical prote |
| 690 | 66 | 5.5 | 508 | 2 | G47677 | hypothetical prote |
| 691 | 66 | 5.5 | 525 | 2 | T28306 | ORF MSV145 hypothe |
| 692 | 66 | 5.5 | 527 | 2 | G69635 | PTS arbutin-like e |
| 693 | 66 | 5.5 | 532 | 2 | A90037 | hypothetical prote |
| 694 | 66 | 5.5 | 546 | 2 | A69890 | hypothetical prote |
| 695 | 66 | 5.5 | 548 | 2 | B87423 | cytochrome-c oxida |
| 696 | 66 | 5.5 | 552 | 2 | S45886 | hypothetical prote |
| 697 | 66 | 5.5 | 565 | 2 | S73707 | Na(+) translocatin |
| 698 | 66 | 5.5 | 570 | 2 | S07744 | hypothetical prote |
| 699 | 66 | 5.5 | 573 | 1 | S33212 | INDAl protein - fu |
| 700 | 66 | 5.5 | 573 | 2 | AF1418 | NADH2 dehydrogenas |
| 701 | 66 | 5.5 | 573 | 2 | AH1793 | ABC transporter, A |
| 702 | 66 | 5.5 | 619 | 2 | T11314 | ABC transporter, A |
| 703 | 66 | 5.5 | 632 | 2 | T24405 | hypothetical prote |
| 704 | 66 | 5.5 | 654 | 2 | A98350 | hypothetical ABC t |
| 705 | 66 | 5.5 | 705 | 2 | AF2932 | hypothetical prote |
| 706 | 66 | 5.5 | 721 | 2 | T48464 | hypothetical prote |
| 707 | 66 | 5.5 | 736 | 2 | A70764 | probable GlgX prot |
| 708 | 66 | 5.5 | 784 | 2 | G01522 | acidic 82 kDa prot |
| 709 | 66 | 5.5 | 1039 | 2 | B90442 | tricorn proteinase |
| 710 | 66 | 5.5 | 1054 | 2 | S76747 | probable calcium t |
| 711 | 66 | 5.5 | 146 | 2 | A61221 | hypothetical prote |
| 712 | 66 | 5.5 | 1359 | 2 | T34036 | signal peptidase I |
| 713 | 66 | 5.5 | 1375 | 2 | S48375 | hypothetical prote |
| 714 | 66 | 5.5 | 2599 | 2 | F90608 | hypothetical prote |
| 715 | 66 | 5.5 | 26926 | 1 | I38344 | titin, cardiac mus |
| 716 | 65.5 | 5.5 | 132 | 2 | E97760 | signal sequence pe |
| 717 | 65.5 | 5.5 | 297 | 2 | F69456 | NADH2 dehydrogenas |
| 718 | 65.5 | 5.5 | 301 | 2 | T21308 | phosphate ABC tran |
| 719 | 65.5 | 5.5 | 317 | 2 | S23459 | hypothetical prote |
| 720 | 65.5 | 5.5 | 327 | 2 | T36087 | polysulfide reduct |
| 721 | 65.5 | 5.5 | 348 | 1 | S36003 | probable binding p |
| 722 | 65.5 | 5.5 | 351 | 2 | S67771 | NADH2 dehydrogenas |
| 723 | 65.5 | 5.5 | 365 | 2 | F82880 | hypothetical prote |
| 724 | 65.5 | 5.5 | 367 | 2 | F66629 | hypothetical prote |
| 725 | 65.5 | 5.5 | 297 | 1 | F86839 | phosphate ABC tran |
| 726 | 65.5 | 5.5 | 301 | 2 | B83792 | hypothetical prote |
| 727 | 65.5 | 5.5 | 379 | 2 | E70074 | ubiquinol-cytochro |
| 728 | 65.5 | 5.5 | 327 | 2 | T32778 | hypothetical prote |
| 729 | 65.5 | 5.5 | 391 | 2 | T32601 | NADH2 dehydrogenas |
| 730 | 65.5 | 5.5 | 351 | 2 | S36003 | hypothetical ferri |
| 731 | 65.5 | 5.5 | 365 | 1 | F82880 | spore germination |
| 732 | 65.5 | 5.5 | 367 | 2 | JC2056 | prostaglandin E2 r |
| 733 | 65.5 | 5.5 | 379 | 2 | S58456 | ubiquinol-cytochro |
| 734 | 65.5 | 5.5 | 445 | 2 | T38916 | hypothetical prote |
| 735 | 65.5 | 5.5 | 391 | 2 | H83629 | hypothetical prote |
| 736 | 65.5 | 5.5 | 394 | 2 | AH0362 | nucleoside permeas |
| 737 | 65.5 | 5.5 | 410 | 2 | T11064 | NADH2 dehydrogenas |
| 738 | 65.5 | 5.5 | 423 | 2 | E90569 | conserved hypothet |
| 739 | 65.5 | 5.5 | 425 | 2 | AF9688 | hypothetical prote |
| 740 | 65.5 | 5.5 | 425 | 2 | AF2913 | conserved hypothet |
| 741 | 65.5 | 5.5 | 429 | 2 | T32832 | hypothetical prote |
| 742 | 65.5 | 5.5 | 442 | 2 | A42670 | microfibril-associ |
| 743 | 65.5 | 5.5 | 445 | 2 | T38916 | probable transcrip |
| 744 | 65.5 | 5.5 | 449 | 2 | H83629 | probable dicarboxy |
| 745 | 65.5 | 5.5 | 457 | 2 | A75327 | hypothetical prote |
| 746 | 65.5 | 5.5 | 477 | 2 | B75170 | hypothetical prote |
| 747 | 65.5 | 5.5 | 480 | 2 | A60043 | endoplasmic reticu |
| 748 | 65.5 | 5.5 | 487 | 1 | A97928 | type I site-specif |
| 749 | 65.5 | 5.5 | 488 | 2 | H64537 | cytochrome-c oxida |
| 750 | 65.5 | 5.5 | 488 | 2 | G81295 | cytochrome-c oxida |
| 751 | 65.5 | 5.5 | 491 | 2 | AE1197 | efflux transporter |
| 752 | 65.5 | 5.5 | 495 | 2 | A97022 | probably membrane |
| 753 | 65.5 | 5.5 | 500 | 2 | G84706 | hypothetical prote |
| 754 | 65.5 | 5.5 | 502 | 2 | AD3395 | hypothetical prote |
| 755 | 65.5 | 5.5 | 502 | 2 | AD3395 | NADH2 dehydrogenas |
| 756 | 65.5 | 5.5 | 518 | 2 | T25669 | NADH2 dehydrogenas |
| 757 | 65.5 | 5.5 | 528 | 2 | A53207 | probable folate tr |
| 758 | 65.5 | 5.5 | 544 | 2 | T34417 | delayed rectifier |
| 759 | 65.5 | 5.5 | 545 | 2 | B84825 | probable ABC trans |
|  |  |  |  |  | E90460 | hypothetical prote |
| 760 | 65.5 | 5.5 | 561 | 2 | S71189 | Dwarf1 protein - A |
| 761 | 65.5 | 5.5 | 575 | 2 | AH1417 | ABC transporter (A |
| 762 | 65.5 | 5.5 | 578 | 2 | T15736 | hypothetical prote |
| 763 | 65.5 | 5.5 | 583 | 2 | AH1151 | hypothetical prote |
| 764 | 65.5 | 5.5 | 590 | 2 | C81116 | glycerophosphory1 |
| 765 | 65.5 | 5.5 | 597 | 2 | B82881 | probable sugar epi |
| 766 | 65.5 | 5.5 | 617 | 2 | AB1167 | probable sugar prote |
| 767 | 65.5 | 5.5 | 618 | 2 | ACl204 | phosphotransferase |
| 768 | 65.5 | 5.5 | 642 | 2 | H70331 | phosphotransferase |
| 769 | 65.5 | 5.5 | 718 | 2 | A56851 | ATP-dependent heli |
| 770 | 65.5 | 5.5 | 720 | 2 | H82198 | Na+/myo-inositol c |
| 771 | 65.5 | 5.5 | 721 | 2 | AF1254 | RTX toxin transpor |
| 772 | 65.5 | 5.5 | 740 | 2 | S61568 | penicillin-binding |
| 773 | 65.5 | 5.5 | 860 | 1 | QRHULD | probable membrane |
| 774 | 65.5 | 5.5 | 958 | 2 | AC0204 | LDL receptor precu |
| 775 | 65.5 | 5.5 | 225 | 1 | S41797 | probable integral |
| 776 | 65.5 | 5.5 | 1087 | 2 | MMIHIV | cellulose 1,4-beta |
| 777 | 65.5 | 5.5 | 1328 | 2 | B22999 | TYB protein - yea |
| 778 | 65.5 | 5.5 | 1427 | 2 | S74293 | SRB8 protein - yea |
| 779 | 65.5 | 5.5 | 1581 | 2 | B71636 | hypothetical prote |
| 780 | 65.5 | 5.5 | 1635 | 2 | T32452 | growth response pr |
| 781 | 65.5 | 5.4 | 126 | 2 | AD0340 | hemA concentration |
| 782 | 65 | 5.4 | 149 | 2 | C69393 | transcription regu |
| 783 | 65 | 5.4 | 176 | 1 | Q1AD25 | early E1B 21K prot |
| 784 | 65 | 5.4 | 196 | 1 | O1AD25 | hypothetical prote |
| 785 | 65 | 5.4 | 247 | 2 | I48149 | probable abc tran |
| 786 | 65 | 5.4 | 257 | 2 | B75099 | hypothetical prote |
| 787 | 65 | 5.4 | 259 | 2 | A47112 | hypothetical prote |
| 788 | 65 | 5.4 | 271 | 2 | E89950 | dipeptide abc tran |
| 789 | 65 | 5.4 | 280 | 2 | S38091 | hypothetical prote |
| 790 | 65 | 5.4 | 290 | 2 | T15249 | nitrate transport |
| 791 | 65 | 5.4 | 290 | 1 | H69785 | probable chlorophy |
| 792 | 65 | 5.4 | 291 | 2 | I38879 | cytochrome c oxida |
| 793 | 65 | 5.4 | 307 | 2 | S17414 | cytochrome c oxida |
| 794 | 65 | 5.4 | 313 | 2 | S58461 | branched-chain ami |
| 795 | 65 | 5.4 | 319 | 2 | AE2671 | lysophospholipase |
| 796 | 65 | 5.4 | 322 | 2 | B36125 | hypothetical prote |
| 797 | 65 | 5.4 | 330 | 2 | B64084 | hypothetical prote |
| 798 | 65 | 5.4 | 335 | 2 | D87087 | hypothetical prote |
| 799 | 65 | 5.4 | 338 | 2 | H75068 | hypothetical prote |
| 800 | 65 | 5.4 | 344 | 2 | H75060 | NADH2 dehydrogenas |
| 801 | 65 | 5.4 | 345 | 2 | S50339 | NADH2 dehydrogenas |
| 802 | 65 | 5.4 | 355 | 2 | AD1200 | conserved hypothet |
| 803 | 65 | 5.4 | 359 | 2 | T12361 | NADH2 dehydrogenas |
| 804 | 65 | 5.4 | 362 | 2 | G70200 | mannan endo-1,4-be |
| 805 | 65 | 5.4 | 375 | 2 | T15249 | corticotropin rele |
| 806 | 65 | 5.4 | 379 | 1 | H69785 | ubiquinol-cytochro |
| 807 | 65 | 5.4 | 379 | 2 | I38879 | ubiquinol-cytochro |
| 808 | 65 | 5.4 | 379 | 2 | D34285 | ubiquinol-cytochro |
| 809 | 65 | 5.4 | 382 | 2 | S58455 | ubiquinol-cytochro |
| 810 | 65 | 5.4 | 382 | 1 | D34285 | ubiquinol-cytochro |
| 811 | 65 | 5.4 | 390 | 2 | T11138 | hypothetical prote |
| 812 | 65 | 5.4 | 415 | 2 | C84984 | hypothetical prote |
| 813 | 65 | 5.4 | 438 | 2 | T21532 | probable integral |
| 814 | 65 | 5.4 | 442 | 2 | B81410 | probable MFS trans |
| 815 | 65 | 5.4 | 445 | 2 | A83122 | glucosyltransferas |
| 816 | 65 | 5.4 | 457 | 2 | AD2358 | Ser/Thr protein ki |
| 817 | 65 | 5.4 | 462 | 2 | T28334 | protein T27E9.5 li |
| 818 | 65 | 5.4 | 477 | 2 | B88613 | probable membrane |
| 819 | 65 | 5.4 | 479 | 2 | S54508 | TRK system potassi |
| 820 | 65 | 5.4 | 481 | 2 | A69036 | cytochrome-c oxida |
| 821 | 65 | 5.4 | 490 | 2 | E81050 | cytochrome-c oxida |
| 822 | 65 | 5.4 | 492 | 2 | T14545 | NADH2 dehydrogenas |
| 823 | 65 | 5.4 | 510 | 2 | S59107 | probable sugar tra |
| 824 | 65 | 5.4 | 511 | 2 | S55204 | hypothetical prote |
| 825 | 65 | 5.4 | 513 | 2 | H75097 | polysaccharide bio |
| 826 | 65 | 5.4 | 526 | 2 | T37180 | probable membrane |
| 827 | 65 | 5.4 | 530 | 2 | D91047 | hydrogenase 4 memb |
| 828 | 65 | 5.4 | 530 | 1 | A64697 | conserved hypothet |
| 829 | 65 | 5.4 | 535 | 2 | B89771 | hypothetical prote |
| 830 | 65 | 5.4 | 539 | 2 | S55190 | hypothetical prote |
| 831 | 65 | 5.4 | 547 | 2 | T31543 | SNG1 protein - yea |
| 832 | 65 | 5.4 | 576 | 2 | T25375 | hypothetical prote |

| # | | | Len | N | Accession | Description |
|---|---|---|---|---|---|---|
| 833 | 65 | 5.4 | 579 | 2 | S61131 | probable membrane |
| 834 | 65 | 5.4 | 608 | 2 | S65298 | dicarboxylic amino |
| 835 | 65 | 5.4 | 611 | 2 | T21747 | hypothetical prote |
| 836 | 65 | 5.4 | 624 | 2 | G82508 | hypothetical prote |
| 837 | 65 | 5.4 | 627 | 2 | T11125 | NADH2 dehydrogenas |
| 838 | 65 | 5.4 | 633 | 2 | F84483 | NADH2 dehydrogenas |
| 839 | 65 | 5.4 | 638 | 2 | D69957 | Mutator-like trans |
| 840 | 65 | 5.4 | 643 | 2 | F97787 | conserved hypothet |
| 841 | 65 | 5.4 | 676 | 2 | A45515 | sodium/pantothenat |
| 842 | 65 | 5.4 | 684 | 2 | F86394 | dnaK-type molecula |
| 843 | 65 | 5.4 | 697 | 2 | H84791 | protein T24P13.20 |
| 844 | 65 | 5.4 | 702 | 2 | T13505 | hypothetical prote |
| 845 | 65 | 5.4 | 705 | 2 | T04400 | NADH2 dehydrogenas |
| 846 | 65 | 5.4 | 773 | 2 | H96818 | NADH2 dehydrogenas |
| 847 | 65 | 5.4 | 773 | 2 | G83816 | hypothetical prote |
| 848 | 65 | 5.4 | 808 | 2 | T04459 | late competence op |
| 849 | 65 | 5.4 | 861 | 2 | S77086 | hypothetical prote |
| 850 | 65 | 5.4 | 927 | 2 | T38518 | ribonuclease II RN |
| 851 | 65 | 5.4 | 931 | 2 | F84637 | probable plasma me |
| 852 | 65 | 5.4 | 938 | 2 | T01809 | hypothetical prote |
| 853 | 65 | 5.4 | 1089 | 2 | C70522 | probable mmpL8 pro |
| 854 | 65 | 5.4 | 1163 | 2 | D64315 | type I restriction |
| 855 | 65 | 5.4 | 1178 | 2 | S76370 | anion exchanger 3 |
| 856 | 65 | 5.4 | 1232 | 2 | I38496 | sensory transducti |
| 857 | 65 | 5.4 | 1421 | 2 | T34225 | hypothetical prote |
| 858 | 65 | 5.4 | 5069 | 2 | T17464 | rifamycin polyketi |
| 859 | 65 | 5.4 | 180 | 2 | T41339 | hypothetical prote |
| 860 | 64.5 | 5.4 | 211 | 2 | S35280 | eaC protein - phag |
| 861 | 64.5 | 5.4 | 217 | 2 | AE0395 | probable amino aci |
| 862 | 64.5 | 5.4 | 227 | 2 | C69432 | hypothetical prote |
| 863 | 64.5 | 5.4 | 234 | 2 | E96957 | HAD superfamily hy |
| 864 | 64.5 | 5.4 | 268 | 2 | AF2470 | potassium channel |
| 865 | 64.5 | 5.4 | 271 | 2 | E81384 | prolipoprotein dia |
| 866 | 64.5 | 5.4 | 275 | 2 | T43119 | hypothetical prote |
| 867 | 64.5 | 5.4 | 293 | 2 | D71517 | probable metal tra |
| 868 | 64.5 | 5.4 | 295 | 2 | T32202 | hypothetical prote |
| 869 | 64.5 | 5.4 | 297 | 2 | T27584 | hypothetical prote |
| 870 | 64.5 | 5.4 | 320 | 2 | T23904 | hypothetical prote |
| 871 | 64.5 | 5.4 | 326 | 2 | A86411 | protein F3M18.6 [i |
| 872 | 64.5 | 5.4 | 353 | 2 | F64175 | hypothetical prote |
| 873 | 64.5 | 5.4 | 358 | 2 | T22823 | hypothetical prote |
| 874 | 64.5 | 5.4 | 361 | 2 | A86841 | hypothetical prote |
| 875 | 64.5 | 5.4 | 361 | 1 | A40734 | Pas (passover) pro |
| 876 | 64.5 | 5.4 | 379 | 1 | S43264 | ubiquinol-cytochro |
| 877 | 64.5 | 5.4 | 379 | 2 | T11505 | ubiquinol-cytochro |
| 878 | 64.5 | 5.4 | 379 | 2 | S58454 | ubiquinol-cytochro |
| 879 | 64.5 | 5.4 | 379 | 2 | A53077 | ubiquinol-cytochro |
| 880 | 64.5 | 5.4 | 381 | 1 | CBMS | ubiquinol-cytochro |
| 881 | 64.5 | 5.4 | 381 | 2 | S33449 | pituitary adenylat |
| 882 | 64.5 | 5.4 | 385 | 2 | H69154 | hypothetical prote |
| 883 | 64.5 | 5.4 | 398 | 2 | H95057 | NADH2 dehydrogenas |
| 884 | 64.5 | 5.4 | 398 | 2 | A97927 | phosphoglycerate k |
| 885 | 64.5 | 5.4 | 400 | 2 | G01977 | d3 dopamine recept |
| 886 | 64.5 | 5.4 | 411 | 2 | S46800 | LAG1 protein - yea |
| 887 | 64.5 | 5.4 | 416 | 2 | AF1127 | rod shape-determin |
| 888 | 64.5 | 5.4 | 426 | 2 | T45800 | UDP-N-acetylglucos |
| 889 | 64.5 | 5.4 | 433 | 2 | T11162 | NADH2 dehydrogenas |
| 890 | 64.5 | 5.4 | 435 | 2 | AC0105 | probable maltodext |
| 891 | 64.5 | 5.4 | 439 | 2 | C22845 | hypothetical prote |
| 892 | 64.5 | 5.4 | 439 | 2 | A84153 | NADH2 dehydrogenas |
| 893 | 64.5 | 5.4 | 443 | 2 | B26696 | hypothetical prote |
| 894 | 64.5 | 5.4 | 444 | 2 | T11474 | NADH2 dehydrogenas |
| 895 | 64.5 | 5.4 | 444 | 2 | A43676 | hypothetical prote |
| 896 | 64.5 | 5.4 | 444 | 1 | A48218 | dopamine receptor |
| 897 | 64.5 | 5.4 | 446 | 2 | DYRTD3 | microtubular aggre |
| 898 | 64.5 | 5.4 | 448 | 2 | D85362 | hypothetical prote |
| 899 | 64.5 | 5.4 | 448 | 2 | S57909 | P44 hepatitis-asso |
| 900 | 64.5 | 5.4 | 450 | 2 | T23528 | probable histidine |
| 901 | 64.5 | 5.4 | 451 | 2 | D70045 | hypothetical prote |
| 902 | 64.5 | 5.4 | 467 | 2 | JN0616 | two-component sens |
| 903 | 64.5 | 5.4 | 478 | 1 | C29051 | pituitary adenylat |
| 904 | 64.5 | 5.4 | 495 | 2 | FWSYG2 | transposase C - Ba |
| 905 | 65 | 5.4 | 495 | 2 | S39061 | glycinin chain Ala |
| 906 | 64.5 | 5.4 | 495 | 2 | S36114 | pituitary adenylat |
| 907 | 64.5 | 5.4 | 495 | 2 | S10851 | glycinin G1 precur |
| 908 | 64.5 | 5.4 | 512 | 2 | H64964 | probable membrane |
| 909 | 64.5 | 5.4 | 521 | 2 | A99549 | amino acid permeas |
| 910 | 64.5 | 5.4 | 523 | 2 | S39060 | pituitary adenylyl |
| 911 | 64.5 | 5.4 | 547 | 2 | H65107 | hypothetical prote |
| 912 | 64.5 | 5.4 | 554 | 2 | A56730 | cat1 protein 61.6 |
| 913 | 64.5 | 5.4 | 575 | 2 | B97812 | virulence factor m |
| 914 | 64.5 | 5.4 | 575 | 2 | A81793 | ABC transporter (A |
| 915 | 64.5 | 5.4 | 576 | 2 | T05904 | cytochrome P450 97 |
| 916 | 64.5 | 5.4 | 614 | 2 | B99869 | hypothetical prote |
| 917 | 64.5 | 5.4 | 622 | 2 | AC1236 | acyltransferase (t |
| 918 | 64.5 | 5.4 | 638 | 1 | QOBY2M | mRNA maturase bI4 |
| 919 | 64.5 | 5.4 | 715 | 2 | T26307 | hypothetical prote |
| 920 | 64.5 | 5.4 | 720 | 2 | T47648 | ABC transporter-li |
| 921 | 64.5 | 5.4 | 721 | 2 | AD1617 | penicillin-binding |
| 922 | 64.5 | 5.4 | 721 | 2 | AE1491 | hypothetical prote |
| 923 | 64.5 | 5.4 | 735 | 2 | AD0341 | probable membrane |
| 924 | 64.5 | 5.4 | 763 | 2 | AD1070 | phosphatidylglycer |
| 925 | 64.5 | 5.4 | 801 | 2 | A89862 | Na+/H+ antiporter |
| 926 | 64.5 | 5.4 | 803 | 2 | H64568 | histidine kinase - |
| 927 | 64.5 | 5.4 | 889 | 2 | T30715 | probable major cor |
| 928 | 64.5 | 5.4 | 979 | 2 | A70848 | probable membrane |
| 929 | 64 | 5.4 | 1007 | 2 | JC8066 | 125K surface antig |
| 930 | 64.5 | 5.4 | 1114 | 2 | B70723 | 138K protein - Tet |
| 931 | 64.5 | 5.4 | 1146 | 2 | T48829 | probable mmpl12 pr |
| 932 | 64.5 | 5.4 | 1154 | 2 | T20271 | related to SREBP c |
| 933 | 64.5 | 5.4 | 1465 | 2 | S45628 | DNA-directed DNA p |
| 934 | 64.5 | 5.4 | 1529 | 2 | S69688 | hypothetical prote |
| 935 | 64.5 | 5.4 | 1630 | 2 | S64403 | probable F1G36.3 [i |
| 936 | 64.5 | 5.4 | 1661 | 2 | S64800 | ESP1 protein - yea |
| 937 | 64.5 | 5.4 | 3033 | 1 | GNWVJ8 | probable membrane |
| 938 | 64 | 5.4 | 202 | 2 | A70041 | genome polyprotein |
| 939 | 64 | 5.4 | 209 | 2 | G82359 | conserved hypothet |
| 940 | 64 | 5.4 | 253 | 2 | A70040 | conserved hypothet |
| 941 | 64 | 5.4 | 259 | 2 | T12451 | cdd3 protein - Clo |
| 942 | 64 | 5.4 | 269 | 2 | H69768 | hypothetical prote |
| 943 | 64 | 5.4 | 270 | 2 | F89632 | plant-metabolite d |
| 944 | 64 | 5.4 | 274 | 2 | T50567 | probable ABC-type |
| 945 | 64 | 5.4 | 276 | 2 | C70040 | probable membrane |
| 946 | 64 | 5.4 | 281 | 2 | S48358 | probable sugar upt |
| 947 | 64 | 5.4 | 283 | 2 | C95932 | probable permease |
| 948 | 64 | 5.4 | 285 | 2 | D83009 | sugar transport sy |
| 949 | 64 | 5.4 | 288 | 2 | B83883 | cytochrome-c oxida |
| 950 | 64 | 5.4 | 330 | 2 | S36955 | hypothetical prote |
| 951 | 64 | 5.4 | 342 | 2 | T29675 | dopamine receptor |
| 952 | 64 | 5.4 | 347 | 2 | A48258 | ubiquinol-cytochro |
| 953 | 64 | 5.4 | 351 | 2 | T11248 | NADH2 dehydrogenas |
| 954 | 64 | 5.4 | 351 | 1 | T11419 | protein kinase SPK |
| 955 | 64 | 5.4 | 367 | 1 | S26163 | PL6 protein - huma |
| 956 | 64 | 5.4 | 369 | 1 | S43263 | hypothetical prote |
| 957 | 64 | 5.4 | 379 | 2 | S58452 | hypothetical prote |
| 958 | 64 | 5.4 | 379 | 2 | H90587 | ubiquinol-cytochro |
| 959 | 64 | 5.4 | 379 | 2 | S26031 | ubiquinol-cytochro |
| 960 | 64 | 5.4 | 379 | 2 | G82656 | G protein-coupled |
| 961 | 64 | 5.4 | 379 | 2 | D64181 | NA+/H+ antiporter |
| 962 | 64 | 5.4 | 379 | 2 | S17419 | probable na+/h+ an |
| 963 | 64 | 5.4 | 383 | 2 | S26163 | hypothetical prote |
| 964 | 64 | 5.4 | 383 | 2 | G64667 | drug-efflux transp |
| 965 | 64 | 5.4 | 387 | 2 | H71848 | acyltransferase [i |
| 966 | 64 | 5.4 | 379 | 2 | S74522 | hypothetical prote |
| 967 | 64 | 5.4 | 383 | 2 | AD1417 | ubiquinol-cytochro |
| 968 | 64 | 5.4 | 383 | 2 | S55594 | ubiquinol-cytochro |
| 969 | 64 | 5.4 | 379 | 1 | G01430 | ubiquinol-cytochro |
| 970 | 64 | 5.4 | 379 | 2 | S56716 | ubiquinol-cytochro |
| 971 | 64 | 5.4 | 379 | 2 | A97759 | ubiquinol-cytochro |
| 972 | 64 | 5.4 | 402 | 2 | AE2779 | probable cytochrom |
| 973 | 64 | 5.4 | 404 | 2 | S26021 | twitching motility |
| 974 | 64 | 5.4 | 404 | 2 | S26021 | ubiquinol-cytochro |
| 975 | 64 | 5.4 | 409 | 2 | A55610 | dopamine receptor |
| 976 | 64 | 5.4 | 413 | 2 | H81659 | hypothetical prote |
| 977 | 64 | 5.4 | 413 | 2 | CBBO | NADH2 dehydrogenas |
| 978 | 64 | 5.4 | 422 | 2 | E84338 | corticotropin-rele |

| ID | | | | | Code | Description |
|---|---|---|---|---|---|---|
| 979 | 64 | 5.4 | 430 | 1 | S32570 | malC protein - Str |
| 980 | 64 | 5.4 | 450 | 2 | B40392 | alpha-2-adrenergic |
| 981 | 64 | 5.4 | 451 | 2 | A36908 | spore cortex penic |
| 982 | 64 | 5.4 | 455 | 2 | T31258 | aromatic oxygenase |
| 984 | 64 | 5.4 | 457 | 2 | AF2975 | aminotransferase, |
| 985 | 64 | 5.4 | 457 | 2 | E98307 | hypothetical proce |
| 985 | 64 | 5.4 | 463 | 2 | AC0281 | probable amino aci |
| 986 | 64 | 5.4 | 469 | 2 | H90322 | polysaccharide bio |
| 987 | 64 | 5.4 | 492 | 2 | E58931 | NADH2 dehydrogenas |
| 988 | 64 | 5.4 | 503 | 2 | JC7627 | cytochrome P450 3A |
| 989 | 64 | 5.4 | 511 | 2 | T40334 | hypothetical proce |
| 990 | 64 | 5.4 | 527 | 2 | A75122 | sodium- and chlori |
| 991 | 64 | 5.4 | 536 | 2 | T36109 | hypothetical proce |
| 992 | 64 | 5.4 | 538 | 2 | C90406 | conserved hypothet |
| 993 | 64 | 5.4 | 544 | 2 | T13877 | NADH2 dehydrogenas |
| 994 | 64 | 5.4 | 562 | 2 | T52481 | cytochrome-c oxida |
| 995 | 64 | 5.4 | 575 | 2 | G75282 | probable glutathio |
| 996 | 64 | 5.4 | 586 | 1 | A34400 | ezrin [validated] |
| 997 | 64 | 5.4 | 598 | 2 | T05130 | hypothetical proce |
| 998 | 64 | 5.4 | 602 | 2 | C75120 | hypothetical proce |
| 999 | 64 | 5.4 | 606 | 2 | B69805 | conserved hypothet |
| 1000 | 64 | 5.4 | 606 | 2 | G02640 | polycystic kidney |
| 1001 | 64 | 5.4 | 608 | 2 | F70512 | probable ATPase - |
| 1002 | 64 | 5.4 | 609 | 2 | S37049 | H+-exporting ATPas |
| 1003 | 64 | 5.4 | 614 | 2 | A69845 | Na+/H+ antiporter |
| 1004 | 64 | 5.4 | 630 | 2 | T47177 | DNA ligase (NAD) ( |
| 1005 | 64 | 5.4 | 654 | 2 | C86677 | hypothetical proce |
| 1006 | 64 | 5.4 | 657 | 2 | T52460 | non-phototropic hy |
| 1007 | 64 | 5.4 | 661 | 2 | T51779 | hypothetical proce |
| 1008 | 64 | 5.4 | 674 | 2 | T50347 | hypothetical proce |
| 1009 | 64 | 5.4 | 696 | 2 | AB1566 | hypothetical proce |
| 1010 | 64 | 5.4 | 748 | 2 | T10651 | protein C43E11.11 |
| 1011 | 64 | 5.4 | 802 | 2 | A87754 | hypothetical proce |
| 1012 | 64 | 5.4 | 838 | 2 | H82939 | conserved hypothet |
| 1013 | 64 | 5.4 | 860 | 2 | T37768 | probable vacuolar |
| 1014 | 64 | 5.4 | 874 | 2 | B86322 | F6A14.8 protein - |
| 1015 | 64 | 5.4 | 896 | 2 | AF1409 | probable ATPase - |
| 1016 | 64 | 5.4 | 991 | 2 | S57385 | the two components |
| 1017 | 64 | 5.4 | 1024 | 1 | RNZQBF | probable membrane |
| 1018 | 64 | 5.4 | 1078 | 2 | T19745 | DNA-directed RNA p |
| 1019 | 64 | 5.4 | 1081 | 2 | B81303 | hypothetical proce |
| 1020 | 64 | 5.4 | 1227 | 2 | A33638 | probable membrane |
| 1021 | 64 | 5.4 | 1385 | 2 | T13415 | erythrocyte anion |
| 1022 | 64 | 5.4 | 1462 | 1 | DJHUAC | hypothetical proce |
| 1023 | 64 | 5.4 | 1695 | 2 | JE0084 | DNA-directed DNA p |
| 1024 | 64 | 5.4 | 2496 | 2 | A71616 | voltage-gated sodi |
| 1025 | 63.5 | 5.3 | 111 | 2 | S43115 | secreted protein P |
| 1026 | 63.5 | 5.3 | 123 | 2 | G71692 | acidic ribosomal p |
| 1027 | 63.5 | 5.3 | 147 | 2 | AH0495 | NADH2 dehydrogenas |
| 1028 | 63.5 | 5.3 | 149 | 2 | H70581 | probable membrane |
| 1029 | 63.5 | 5.3 | 195 | 2 | E71000 | hypothetical proce |
| 1030 | 63.5 | 5.3 | 214 | 2 | C90191 | hypothetical proce |
| 1031 | 63.5 | 5.3 | 218 | 2 | B71925 | conserved hypothet |
| 1032 | 63.5 | 5.3 | 218 | 2 | T29205 | cag island protein |
| 1033 | 63.5 | 5.3 | 231 | 2 | F85679 | hypothetical proce |
| 1034 | 63.5 | 5.3 | 238 | 2 | S75336 | probable antirepre |
| 1035 | 63.5 | 5.3 | 241 | 2 | F86691 | ABC transporter pe |
| 1036 | 63.5 | 5.3 | 242 | 2 | S74794 | hypothetical proce |
| 1037 | 63.5 | 5.3 | 246 | 2 | AD3574 | hypothetical proce |
| 1038 | 63.5 | 5.3 | 259 | 2 | AF0106 | branched-chain ami |
| 1039 | 63.5 | 5.3 | 275 | 2 | E95161 | probable membrane |
| 1040 | 63.5 | 5.3 | 275 | 2 | D98027 | hypothetical proce |
| 1041 | 63.5 | 5.3 | 276 | 2 | G84320 | hypothetical proce |
| 1042 | 63.5 | 5.3 | 276 | 2 | E96951 | conserved membrane |
| 1043 | 63.5 | 5.3 | 280 | 2 | T16240 | hypothetical proce |
| 1044 | 63.5 | 5.3 | 282 | 2 | E83086 | conserved hypothet |
| 1045 | 63.5 | 5.3 | 282 | 2 | AB0346 | probable ABC trans |
| 1046 | 63.5 | 5.3 | 291 | 2 | AB2939 | hypothetical proce |
| 1047 | 63.5 | 5.3 | 291 | 2 | E98343 | hypothetical proce |
| 1048 | 63.5 | 5.3 | 291 | 2 | F75571 | hypothetical proce |
| 1049 | 63.5 | 5.3 | 313 | 2 | D26696 | NADH2 dehydrogenas |
| 1050 | 63.5 | 5.3 | 315 | 2 | E69365 | hypothetical proce |
| 1051 | 63.5 | 5.3 | 316 | 2 | H86665 | ferrichrome ABC tr |
| 1052 | 63.5 | 5.3 | 327 | 2 | S56162 | MDCR15 protein - h |
| 1053 | 63.5 | 5.3 | 328 | 2 | D98224 | oligopeptide ABC t |
| 1054 | 63.5 | 5.3 | 328 | 2 | T39824 | septin homolog - f |
| 1055 | 63.5 | 5.3 | 334 | 2 | B72393 | oligopeptide ABC t |
| 1056 | 63.5 | 5.3 | 334 | 2 | T41037 | hypothetical proce |
| 1057 | 63.5 | 5.3 | 334 | 2 | T27081 | hypothetical proce |
| 1058 | 63.5 | 5.3 | 342 | 2 | A38908 | spa40 protein - Sh |
| 1059 | 63.5 | 5.3 | 344 | 2 | T34981 | hypothetical proce |
| 1060 | 63.5 | 5.3 | 355 | 2 | T15203 | probable integral |
| 1061 | 63.5 | 5.3 | 359 | 2 | D90172 | hypothetical proce |
| 1062 | 63.5 | 5.3 | 361 | 2 | AE30771 | hypothetical proce |
| 1063 | 63.5 | 5.3 | 365 | 2 | AB34494 | oligopeptide trans |
| 1064 | 63.5 | 5.3 | 372 | 2 | S26667 | G protein-coupled |
| 1065 | 63.5 | 5.3 | 377 | 2 | B72275 | probable aspartate |
| 1066 | 63.5 | 5.3 | 380 | 1 | CBRT | probable apparatate |
| 1067 | 63.5 | 5.3 | 381 | 2 | B95080 | cell division peri |
| 1068 | 63.5 | 5.3 | 387 | 2 | D81397 | phosphoglycerate k |
| 1069 | 63.5 | 5.3 | 389 | 2 | C71682 | ubiquinol-cytochro |
| 1070 | 63.5 | 5.3 | 392 | 2 | B81358 | ubiquinol-cytochro |
| 1071 | 63.5 | 5.3 | 398 | 2 | H71520 | protein K10B4.2 [i |
| 1072 | 63.5 | 5.3 | 398 | 2 | T33299 | hypothetical proce |
| 1073 | 63.5 | 5.3 | 398 | 2 | A96268 | probable hth trans |
| 1074 | 63.5 | 5.3 | 400 | 2 | G75133 | transmembrane tran |
| 1075 | 63.5 | 5.3 | 404 | 1 | H88012 | ubiquinol-cytochro |
| 1076 | 63.5 | 5.3 | 401 | 2 | T19887 | probable periplasm |
| 1077 | 63.5 | 5.3 | 400 | 2 | LABECA | cell division prot |
| 1078 | 63.5 | 5.3 | 406 | 2 | T46306 | phosphoglycerate k |
| 1079 | 63.5 | 5.3 | 423 | 2 | T04915 | hypothetical proce |
| 1080 | 63.5 | 5.3 | 423 | 2 | C85255 | latent membrane pr |
| 1081 | 63.5 | 5.3 | 426 | 2 | G85255 | hypothetical proce |
| 1082 | 63.5 | 5.3 | 426 | 2 | A96268 | CDP-diacylglycerol |
| 1083 | 63.5 | 5.3 | 438 | 2 | A82262 | CDP-diacylglycerol |
| 1084 | 63.5 | 5.3 | 444 | 2 | B85789 | phosphoglycerate k |
| 1085 | 63.5 | 5.3 | 444 | 2 | B81358 | conserved hypothet |
| 1086 | 63.5 | 5.3 | 445 | 2 | T16025 | hypothetical proce |
| 1087 | 63.5 | 5.3 | 447 | 2 | F90940 | hypothetical proce |
| 1088 | 63.5 | 5.3 | 447 | 2 | S52437 | CDP-diacylglycerol |
| 1089 | 63.5 | 5.3 | 450 | 2 | T21118 | CDP-diacylglycerol |
| 1090 | 63.5 | 5.3 | 452 | 2 | E96738 | hypothetical proce |
| 1091 | 63.5 | 5.3 | 461 | 2 | C97187 | hypothetical proce |
| 1092 | 63.5 | 5.3 | 468 | 2 | T48686 | sugar transferase |
| 1093 | 63.5 | 5.3 | 487 | 2 | H90562 | hypothetical proce |
| 1094 | 63.5 | 5.3 | 487 | 2 | B95059 | mg2+ transport pro |
| 1095 | 63.5 | 5.3 | 491 | 2 | A64939 | hypothetical proce |
| 1096 | 63.5 | 5.3 | 492 | 2 | S76516 | sugar transport re |
| 1097 | 63.5 | 5.3 | 494 | 2 | F90373 | integral membrane |
| 1098 | 63.5 | 5.3 | 494 | 2 | T48385 | transporter like p |
| 1099 | 63.5 | 5.3 | 498 | 2 | T16190 | hypothetical proce |
| 1100 | 63.5 | 5.3 | 498 | 2 | AF23325 | NADH dehydrogenase |
| 1101 | 63.5 | 5.3 | 500 | 2 | G90321 | hypothetical proce |
| 1102 | 63.5 | 5.3 | 511 | 2 | A70201 | virulence factor m |
| 1103 | 63.5 | 5.3 | 512 | 1 | G82873 | nucleocapsid prote |
| 1104 | 63.5 | 5.3 | 512 | 2 | A49601 | conserved hypothet |
| 1105 | 63.5 | 5.3 | 525 | 2 | 149454 | sterol O-acyltrans |
| 1106 | 63.5 | 5.3 | 537 | 2 | C96943 | uncharacterized me |
| 1107 | 63.5 | 5.3 | 544 | 2 | E64537 | l-lactate permease |
| 1108 | 63.5 | 5.3 | 551 | 2 | G96744 | probable peptide t |
| 1109 | 63.5 | 5.3 | 551 | 2 | D71969 | probable L-lactate |
| 1110 | 63.5 | 5.3 | 555 | 2 | C75340 | l-lactate permease |
| 1111 | 63.5 | 5.3 | 567 | 2 | T17588 | hyaluronoglucosami |
| 1112 | 63.5 | 5.3 | 568 | 2 | 146528 | sodium/dicarboxyla |
| 1113 | 63.5 | 5.3 | 593 | 2 | B88956 | protein ZK697.5 [i |
| 1114 | 63.5 | 5.3 | 594 | 2 | A36361 | glucose transport |
| 1115 | 63.5 | 5.3 | 605 | 2 | H71562 | probable flagellar |
| 1116 | 63.5 | 5.3 | 605 | 2 | T43974 | hypothetical proce |
| 1117 | 63.5 | 5.3 | 605 | 2 | T44161 | hypothetical proce |
| 1118 | 63.5 | 5.3 | 610 | 2 | B54759 | ba-type ubiquinol |
| 1119 | 63.5 | 5.3 | 668 | 2 | B37237 | protein kinase C ( |
| 1120 | 63.5 | 5.3 | 671 | 2 | AF0697 | probable type III |
| 1121 | 63.5 | 5.3 | 681 | 2 | A85044 | hypothetical proce |
| 1122 | 63.5 | 5.3 | 683 | 2 | JQ1148 | killer toxin KHS p |
| 1123 | 63.5 | 5.3 | 708 | 2 | T20148 | hypothetical proce |
| 1124 | 63.5 | 5.3 | 741 | 2 | T48189 | probable transport |
|  | 63.5 | 5.3 | 780 | 2 | A70132 | cell division prot |

| No. | | | Value | | Code | Description |
|---|---|---|---|---|---|---|
| 1125 | 63.5 | 5.3 | 819 | 2 | T19351 | hypothetical prote |
| 1126 | 63.5 | 5.3 | 841 | 2 | T38703 | hypothetical prote |
| 1127 | 63.5 | 5.3 | 843 | 2 | T32487 | hypothetical prote |
| 1128 | 63.5 | 5.3 | 843 | 2 | T41237 | conserved hypothet |
| 1129 | 63.5 | 5.3 | 844 | 2 | A02339 | hypothetical protei |
| 1130 | 63.5 | 5.3 | 951 | 2 | T08987 | probable cadmium-t |
| 1131 | 63.5 | 5.3 | 966 | 2 | H97717 | hypothetical prote |
| 1132 | 63.5 | 5.3 | 1004 | 2 | H97323 | hypothetical prote |
| 1133 | 63.5 | 5.3 | 1098 | 2 | G87323 | hypothetical prote |
| 1134 | 63.5 | 5.3 | 1229 | 2 | S38100 | SlP3 protein - yea |
| 1135 | 63.5 | 5.3 | 1351 | 2 | S42391 | hypothetical prote |
| 1136 | 63.5 | 5.3 | 1388 | 2 | C71607 | hypothetical prote |
| 1137 | 63.5 | 5.3 | 1407 | 2 | T17269 | probable membrane |
| 1138 | 63.5 | 5.3 | 1408 | 1 | T00558 | probable ABC trans |
| 1139 | 63.5 | 5.3 | 1545 | 2 | T47671 | P-glycoprotein-lik |
| 1140 | 63.5 | 5.3 | 1545 | 2 | T42751 | sulfonylurea recep |
| 1141 | 63.5 | 5.3 | 1769 | 2 | T46645 | sulfonylurea recep |
| 1142 | 63.5 | 5.3 | 2357 | 2 | S53378 | probable membrane |
| 1143 | 63.5 | 5.3 | 4725 | 1 | A44357 | dynein heavy chain |
| 1144 | 63 | 5.3 | 96 | 1 | WMVZP3 | F3 protein - fowlp |
| 1145 | 63 | 5.3 | 103 | 1 | T20878 | hypothetical prote |
| 1146 | 63 | 5.3 | 175 | 2 | D70945 | hypothetical prote |
| 1147 | 63 | 5.3 | 230 | 2 | B81705 | conserved hypothet |
| 1148 | 63 | 5.3 | 230 | 2 | T17506 | hypothetical prote |
| 1149 | 63 | 5.3 | 236 | 2 | P83520 | phosphoribosylamin |
| 1150 | 63 | 5.3 | 249 | 2 | T01891 | hypothetical prote |
| 1151 | 63 | 5.3 | 257 | 2 | S01165 | achaete-scute locu |
| 1152 | 63 | 5.3 | 258 | 2 | H65188 | sec-independent pr |
| 1153 | 63 | 5.3 | 258 | 2 | F86071 | sec-independent pr |
| 1154 | 63 | 5.3 | 280 | 2 | H91224 | Sec-independent pr |
| 1155 | 63 | 5.3 | 280 | 2 | D84015 | maltose/maltodextr |
| 1156 | 63 | 5.3 | 288 | 2 | S36954 | geranylgeranyl tra |
| 1157 | 63 | 5.3 | 290 | 2 | S48301 | cytochrome-c oxida |
| 1158 | 63 | 5.3 | 301 | 2 | T50001 | hypothetical prote |
| 1159 | 63 | 5.3 | 306 | 2 | T01891 | hypothetical prote |
| 1160 | 63 | 5.3 | 313 | 2 | H83620 | probable permease |
| 1161 | 63 | 5.3 | 322 | 2 | A86743 | hypothetical prote |
| 1162 | 63 | 5.3 | 329 | 2 | B90013 | hypothetical prote |
| 1163 | 63 | 5.3 | 332 | 2 | B87790 | protein B0207.4 [i |
| 1164 | 63 | 5.3 | 339 | 2 | B84943 | conserved hypothet |
| 1165 | 63 | 5.3 | 345 | 2 | B89880 | hypothetical prote |
| 1166 | 63 | 5.3 | 358 | 2 | T12364 | NADH2 dehydrogenas |
| 1167 | 63 | 5.3 | 359 | 2 | S56720 | probable serine/th |
| 1168 | 63 | 5.3 | 361 | 2 | B83808 | probable serine/th |
| 1169 | 63 | 5.3 | 362 | 2 | A45211 | surface adhesion h |
| 1170 | 63 | 5.3 | 362 | 2 | C69804 | hypothetical prote |
| 1171 | 63 | 5.3 | 364 | 2 | T29552 | prostaglandin E re |
| 1172 | 63 | 5.3 | 365 | 2 | A42414 | prostaglandin E re |
| 1173 | 63 | 5.3 | 378 | 1 | S17412 | prostaglandin E re |
| 1174 | 63 | 5.3 | 379 | 1 | S17411 | ubiquinol-cytochro |
| 1175 | 63 | 5.3 | 379 | 1 | S41833 | ubiquinol-cytochro |
| 1176 | 63 | 5.3 | 379 | 1 | S41847 | ubiquinol-cytochro |
| 1177 | 63 | 5.3 | 379 | 1 | S43265 | ubiquinol-cytochro |
| 1178 | 63 | 5.3 | 379 | 2 | T11492 | ubiquinol-cytochro |
| 1179 | 63 | 5.3 | 379 | 2 | S65009 | ubiquinol-cytochro |
| 1180 | 63 | 5.3 | 379 | 2 | S47882 | ubiquinol-cytochro |
| 1181 | 63 | 5.3 | 382 | 2 | S58464 | NADH2 dehydrogenas |
| 1182 | 63 | 5.3 | 386 | 2 | S58085 | aromatic amino aci |
| 1183 | 63 | 5.3 | 389 | 2 | T11492 | aspartate transami |
| 1184 | 63 | 5.3 | 389 | 2 | H95003 | molybdopterin bios |
| 1185 | 63 | 5.3 | 391 | 2 | S60646 | cell division prot |
| 1186 | 63 | 5.3 | 396 | 2 | C97876 | proton/sodium-glut |
| 1187 | 63 | 5.3 | 398 | 2 | D64541 | hypothetical prote |
| 1188 | 63 | 5.3 | 405 | 2 | E97947 | arsenite transport |
| 1189 | 63 | 5.3 | 411 | 2 | B70415 | corticotropin-rele |
| 1190 | 63 | 5.3 | 415 | 2 | T20902 | cyclin Ia - maize |
| 1191 | 63 | 5.3 | 420 | 2 | G90154 | hypothetical prote |
| 1192 | 63 | 5.3 | 431 | 2 | S39535 | hypothetical prote |
| 1193 | 63 | 5.3 | 448 | 2 | A57742 | alpha-2A-adrenergi |
| 1194 | 63 | 5.3 | 450 | 2 | T30982 | hypothetical prote |
| 1195 | 63 | 5.3 | 469 | 2 | T23809 | hypothetical prote |
| 1196 | 63 | 5.3 | 475 | 2 | S52893 | hypothetical prote |
| 1197 | 63 | 5.3 | 478 | 2 | C59095 | hypothetical prote |
| 1198 | 63 | 5.3 | 480 | 2 | B70367 | hypothetical prote |
| 1199 | 63 | 5.3 | 481 | 2 | S02260 | stomatin-like prot |
| 1200 | 63 | 5.3 | 490 | 2 | C71541 | probable na-depend |
| 1201 | 63 | 5.3 | 491 | 2 | ACL499 | transmembrane prot |
| 1202 | 63 | 5.3 | 493 | 2 | T02376 | hypothetical prote |
| 1203 | 63 | 5.3 | 494 | 2 | T42246 | NADH2 dehydrogenas |
| 1204 | 63 | 5.3 | 494 | 2 | E90594 | amino acid permeas |
| 1205 | 63 | 5.3 | 508 | 1 | A48528 | membrane glycoprot |
| 1206 | 63 | 5.3 | 509 | 2 | E90594 | probable nuclear d |
| 1207 | 63 | 5.3 | 527 | 2 | T40744 | hypothetical prote |
| 1208 | 63 | 5.3 | 531 | 2 | AH1491 | hypothetical prote |
| 1209 | 63 | 5.3 | 533 | 2 | T06153 | hypothetical prote |
| 1210 | 63 | 5.3 | 534 | 2 | A93316 | flagellar basal-bo |
| 1211 | 63 | 5.3 | 534 | 2 | AF1835 | protein Similar to |
| 1212 | 63 | 5.3 | 535 | 2 | B70081 | hypothetical prote |
| 1213 | 63 | 5.3 | 562 | 2 | B86359 | hypothetical prote |
| 1214 | 63 | 5.3 | 565 | 2 | C70136 | hypothetical prote |
| 1215 | 63 | 5.3 | 569 | 2 | T47566 | probable PTR2 fami |
| 1216 | 63 | 5.3 | 574 | 2 | AB2177 | probable membrane- |
| 1217 | 63 | 5.3 | 579 | 2 | G84829 | two-component sens |
| 1218 | 63 | 5.3 | 583 | 2 | G89789 | two-component sens |
| 1219 | 63 | 5.3 | 584 | 2 | B83875 | probable membrane |
| 1220 | 63 | 5.3 | 598 | 2 | S66954 | ABC transporter AT |
| 1221 | 63 | 5.3 | 600 | 2 | T26574 | hypothetical prote |
| 1222 | 63 | 5.3 | 608 | 2 | AD2000 | two-component sens |
| 1223 | 63 | 5.3 | 677 | 2 | F95910 | replication licens |
| 1224 | 63 | 5.3 | 677 | 2 | H64485 | replication licens |
| 1225 | 63 | 5.3 | 682 | 1 | T13568 | protein H64485 [i |
| 1226 | 63 | 5.3 | 701 | 2 | T13665 | NADH2 dehydrogenas |
| 1227 | 63 | 5.3 | 702 | 2 | T12677 | NADH2 dehydrogenas |
| 1228 | 63 | 5.3 | 704 | 2 | H26127 | NADH2 dehydrogenas |
| 1229 | 63 | 5.3 | 712 | 2 | D87418 | proton pump, proba |
| 1230 | 63 | 5.3 | 729 | 2 | T06127 | probable sugar tra |
| 1231 | 63 | 5.3 | 737 | 2 | I39547 | S-protein secretio |
| 1232 | 63 | 5.3 | 738 | 2 | S58612 | S-protein secretio |
| 1233 | 63 | 5.3 | 769 | 2 | G95270 | NADH2 dehydrogenas |
| 1234 | 63 | 5.3 | 813 | 2 | T02672 | NADH2 dehydrogenas |
| 1235 | 63 | 5.3 | 849 | 2 | C87740 | protein H26D21.2 [ |
| 1236 | 63 | 5.3 | 869 | 2 | S49844 | hypothetical prote |
| 1237 | 63 | 5.3 | 943 | 2 | B45082 | hypothetical prote |
| 1238 | 63 | 5.3 | 960 | 2 | T17297 | neurotrophic recep |
| 1239 | 63 | 5.3 | 1030 | 2 | H70360 | neurotrophic recep |
| 1240 | 63 | 5.3 | 1034 | 2 | B86880 | hypothetical prote |
| 1241 | 63 | 5.3 | 1082 | 2 | B82809 | probable membrane |
| 1242 | 63 | 5.3 | 1212 | 2 | B34911 | band 3-related pro |
| 1243 | 63 | 5.3 | 1227 | 2 | T18438 | band 3-related pro |
| 1244 | 63 | 5.3 | 1532 | 2 | S67379 | DNA-damage-inducib |
| 1245 | 63 | 5.3 | 1646 | 2 | JH0422 | type III secretion |
| 1246 | 63 | 5.3 | 1854 | 2 | T39035 | escT [imported] - |
| 1247 | 63 | 5.3 | 2203 | 2 | T42742 | hypothetical prote |
| 1248 | 63 | 5.3 | 2295 | 2 | T22698 | SWI/SNF family hel |
| 1249 | 63 | 5.3 | 4488 | 1 | RRIHM2 | cation efflux syst |
| 1250 | 62.5 | 5.3 | 107 | 2 | F83705 | exodeoxyribonuclea |
| 1251 | 62.5 | 5.3 | 140 | 2 | H70091 | anion exchanger 3, |
| 1252 | 62.5 | 5.3 | 148 | 2 | T20810 | potassium channel |
| 1253 | 62.5 | 5.3 | 168 | 2 | S10658 | potassium channel |
| 1254 | 62.5 | 5.3 | 173 | 2 | JC1169 | hypothetical prote |
| 1255 | 62.5 | 5.3 | 178 | 2 | D71702 | hypothetical prote |
| 1256 | 62.5 | 5.3 | 181 | 2 | JH0422 | voltage-dependent |
| 1257 | 62.5 | 5.3 | 200 | 2 | A71895 | putative sodium ch |
| 1258 | 62.5 | 5.3 | 232 | 2 | G82911 | voltage-dependent |
| 1259 | 62.5 | 5.3 | 236 | 2 | T22698 | hypothetical prote |
| 1260 | 62.5 | 5.3 | 240 | 2 | B71621 | genome polyprotein |
| 1261 | 62.5 | 5.2 | 245 | 2 | B86739 | probable membrane |
| 1262 | 62.5 | 5.2 | 245 | 2 | B83851 | probable membrane |
| 1263 | 62.5 | 5.2 | 258 | 2 | B91201 | hypothetical prote |
| 1264 | 62.5 | 5.2 | 258 | 2 | B86048 | hypothetical prote |
| 1265 | 62.5 | 5.2 | 274 | 2 | AC2946 | hypothetical prote |
| 1266 | 62.5 | 5.2 | 274 | 2 | G98336 | sorbitol/mannitol |
| 1267 | 62.5 | 5.2 | 274 | 2 | G72292 | glycerol-3-phospha |
| 1268 | 62.5 | 5.2 | 276 | 2 | H83568 | hypothetical prote |
| 1269 | 62.5 | 5.2 | 280 | 2 | T24579 | NADH2 dehydrogenas |
| 1270 | 62.5 | 5.2 | 289 | 2 | T11063 | hypothetical prote |

| No | % | E | Len | N | Accession | Description |
|---|---|---|---|---|---|---|
| 1271 | 62.5 | 5.2 | 296 | 2 | H83480 | cytochrome o ubiqu |
| 1272 | 62.5 | 5.2 | 298 | 2 | T37251 | homeobox protein c |
| 1273 | 62.5 | 5.2 | 299 | 2 | T26365 | hypothetical prote |
| 1274 | 62.5 | 5.2 | 326 | 2 | C90272 | hypothetical prote |
| 1275 | 62.5 | 5.2 | 333 | 2 | AB1925 | hypothetical prote |
| 1276 | 62.5 | 5.2 | 333 | 2 | B89010 | protein R08F11.2 | |
| 1277 | 62.5 | 5.2 | 335 | 2 | T41426 | hypothetical prote |
| 1278 | 62.5 | 5.2 | 349 | 2 | N95060 | ABC transporter, p |
| 1279 | 62.5 | 5.2 | 349 | 2 | D97929 | probable integral |
| 1280 | 62.5 | 5.2 | 352 | 2 | E81450 | hypothetical prote |
| 1281 | 62.5 | 5.2 | 358 | 2 | E83829 | hypothetical prote |
| 1282 | 62.5 | 5.2 | 365 | 2 | F82210 | amino acid ABC tra |
| 1283 | 62.5 | 5.2 | 369 | 2 | C88030 | protein F4F5.10 | |
| 1284 | 62.5 | 5.2 | 370 | 2 | C69309 | conserved hypothet |
| 1285 | 62.5 | 5.2 | 379 | 1 | S17407 | conserved hypothet |
| 1286 | 62.5 | 5.2 | 379 | 2 | S58462 | omega-3 fatty acid |
| 1287 | 62.5 | 5.2 | 379 | 2 | S58057 | hypothetical prote |
| 1288 | 62.5 | 5.2 | 382 | 2 | A72373 | conserved hypothet |
| 1289 | 62.5 | 5.2 | 383 | 1 | A44227 | ubiquinol-cytochro |
| 1290 | 62.5 | 5.2 | 383 | 2 | F84771 | ubiquinol-cytochro |
| 1291 | 62.5 | 5.2 | 383 | 2 | T31738 | hypothetical prote |
| 1292 | 62.5 | 5.2 | 388 | 2 | C64722 | Na+/H+-exchanging |
| 1293 | 62.5 | 5.2 | 391 | 2 | A86632 | hypothetical prote |
| 1294 | 62.5 | 5.2 | 399 | 2 | A86630 | aromatic amino aci |
| 1295 | 62.5 | 5.2 | 404 | 2 | H83249 | hypothetical prote |
| 1296 | 62.5 | 5.2 | 405 | 1 | QBE35 | sodium/glutamate s |
| 1297 | 62.5 | 5.2 | 406 | 2 | H89006 | BBRF3 protein - hu |
| 1298 | 62.5 | 5.2 | 409 | 2 | C89942 | protein T22F3.11 | |
| 1299 | 62.5 | 5.2 | 413 | 2 | AC1369 | conserved hypothet |
| 1300 | 62.5 | 5.2 | 417 | 2 | T51467 | multidrug resistan |
| 1301 | 62.5 | 5.2 | 420 | 2 | D95018 | glucose 6 phosphat |
| 1302 | 62.5 | 5.2 | 420 | 2 | E97891 | conserved hypothet |
| 1303 | 62.5 | 5.2 | 422 | 2 | C70518 | conserved hypothet |
| 1304 | 62.5 | 5.2 | 425 | 2 | E97172 | probable nanT prot |
| 1305 | 62.5 | 5.2 | 426 | 2 | A72080 | flagellin [importe |
| 1306 | 62.5 | 5.2 | 426 | 2 | E86542 | ct266 hypothetical |
| 1307 | 62.5 | 5.2 | 431 | 2 | H84069 | CT266 hypothetical |
| 1308 | 62.5 | 5.2 | 440 | 1 | T20092 | hypothetical prote |
| 1309 | 62.5 | 5.2 | 442 | 2 | JQ1042 | endothelin recepto |
| 1310 | 62.5 | 5.2 | 443 | 2 | F30010 | NADH2 dehydrogenas |
| 1311 | 62.5 | 5.2 | 443 | 2 | T08136 | NADH2 dehydrogenas |
| 1312 | 62.5 | 5.2 | 452 | 2 | G64844 | probable omega-6 d |
| 1313 | 62.5 | 5.2 | 452 | 2 | G85647 | probable membrane |
| 1314 | 62.5 | 5.2 | 452 | 2 | G90787 | hypothetical prote |
| 1315 | 62.5 | 5.2 | 455 | 2 | D97217 | hypothetical prote |
| 1316 | 62.5 | 5.2 | 457 | 2 | F69662 | UDP-N-acetylmuramo |
| 1317 | 62.5 | 5.2 | 459 | 2 | AF3284 | glycosyltransferas |
| 1318 | 62.5 | 5.2 | 461 | 2 | S57713 | high-affinity bran |
| 1319 | 62.5 | 5.2 | 468 | 2 | A49131 | probable mannosyl |
| 1320 | 62.5 | 5.2 | 470 | 2 | C70641 | inositol 1,4,5-tri |
| 1321 | 62.5 | 5.2 | 487 | 2 | S73161 | hypothetical prote |
| 1322 | 62.5 | 5.2 | 490 | 2 | T40116 | hypothetical prote |
| 1323 | 62.5 | 5.2 | 492 | 2 | AC0768 | probable transmemb |
| 1324 | 62.5 | 5.2 | 494 | 2 | T15502 | hypothetical prote |
| 1325 | 62.5 | 5.2 | 501 | 1 | JN0539 | head protein gp5 - |
| 1326 | 62.5 | 5.2 | 502 | 2 | C86263 | hypothetical prote |
| 1327 | 62.5 | 5.2 | 505 | 2 | S44647 | f42h10.1 protein - |
| 1328 | 62.5 | 5.2 | 507 | 2 | S52677 | hypothetical prote |
| 1329 | 62.5 | 5.2 | 546 | 2 | AE0571 | probable membrane |
| 1330 | 62.5 | 5.2 | 547 | 2 | S64332 | probable membrane |
| 1331 | 62.5 | 5.2 | 568 | 2 | S64567 | probable membrane |
| 1332 | 62.5 | 5.2 | 569 | 2 | T22928 | hypothetical prote |
| 1333 | 62.5 | 5.2 | 572 | 2 | T11478 | NADH2 dehydrogenas |
| 1334 | 62.5 | 5.2 | 578 | 2 | I56215 | interleukin-10 rec |
| 1335 | 62.5 | 5.2 | 580 | 2 | TO2596 | interleukin-10 rec |
| 1336 | 62.5 | 5.2 | 601 | 2 | T11451 | NADH2 dehydrogenas |
| 1337 | 62.5 | 5.2 | 608 | 2 | T34391 | hypothetical prote |
| 1338 | 62.5 | 5.2 | 610 | 2 | A28798 | myosin-light-chain |
| 1339 | 62.5 | 5.2 | 621 | 2 | B95897 | probable cellulose |
| 1340 | 62.5 | 5.2 | 638 | 2 | G02068 | white homolog - hu |
| 1341 | 62.5 | 5.2 | 668 | 2 | C71868 | intensifier 1 prot |
| 1342 | 62.5 | 5.2 | 685 | 2 | T04073 | hypothetical prote |
| 1343 | 62.5 | 5.2 | 697 | 2 | T19254 | hypothetical prote |

| No | % | E | Len | N | Accession | Description |
|---|---|---|---|---|---|---|
| 1344 | 62.5 | 5.2 | 704 | 2 | S46000 | probable membrane |
| 1345 | 62.5 | 5.2 | 718 | 2 | T05840 | subtilisin-like pr |
| 1346 | 62.5 | 5.2 | 763 | 2 | T27937 | hypothetical prote |
| 1347 | 62.5 | 5.2 | 807 | 2 | T28279 | ORF MSV119 probabl |
| 1348 | 62.5 | 5.2 | 815 | 2 | G97266 | mannose-1-phosphat |
| 1349 | 62.5 | 5.2 | 837 | 2 | D71027 | hypothetical.prote |
| 1350 | 62.5 | 5.2 | 848 | 2 | A33810 | band 3 anion trans |
| 1351 | 62.5 | 5.2 | 865 | 2 | A33810 | probable membrane |
| 1352 | 62.5 | 5.2 | 881 | 2 | G96574 | hypothetical prote |
| 1353 | 62.5 | 5.2 | 971 | 2 | H71719 | hypothetical prote |
| 1354 | 62.5 | 5.2 | 1082 | 2 | T41988 | probable DNA-direc |
| 1355 | 62.5 | 5.2 | 1144 | 2 | A81983 | hypothetical prote |
| 1356 | 62.5 | 5.2 | 1195 | 2 | C87691 | hypothetical prote |
| 1357 | 62.5 | 5.2 | 1291 | 2 | T17242 | hypothetical prote |
| 1358 | 62.5 | 5.2 | 1291 | 2 | T20642 | protein F09C3.1 [li |
| 1359 | 62.5 | 5.2 | 1397 | 2 | E87998 | hypothetical prote |
| 1360 | 62.5 | 5.2 | 1576 | 2 | T21172 | probable centromer |
| 1361 | 62.5 | 5.2 | 1676 | 2 | E71410 | vitellogenin II pr |
| 1362 | 62.5 | 5.2 | 1687 | 2 | T43144 | protein F3C4. [li |
| 1363 | 62.5 | 5.2 | 1951 | 2 | B43963 | RNA viral polymera |
| 1364 | 62.5 | 5.2 | 2150 | 2 | S13553 | hypothetical prote |
| 1365 | 62.5 | 5.2 | 112 | 2 | T11073 | type 4 prepilin-li |
| 1366 | 62.5 | 5.2 | 132 | 2 | D82954 | NADH2 dehydrogenas |
| 1367 | 62.5 | 5.2 | 174 | 2 | E84028 | hypothetical prote |
| 1368 | 62 | 5.2 | 175 | 1 | IMECB | cell-shape determi |
| 1369 | 62 | 5.2 | 198 | 2 | E97217 | colicin B immunity |
| 1370 | 62 | 5.2 | 201 | 2 | G90134 | uncharacterized co |
| 1371 | 62 | 5.2 | 206 | 2 | P89840 | hypothetical prote |
| 1372 | 62 | 5.2 | 209 | 2 | A88056 | conserved hypothet |
| 1373 | 62 | 5.2 | 209 | 2 | T32573 | protein F37C4. [li |
| 1374 | 62 | 5.2 | 225 | 2 | B65127 | hypothetical prote |
| 1375 | 62 | 5.2 | 247 | 1 | F75433 | type 4 prepilin-li |
| 1376 | 62 | 5.2 | 247 | 2 | AC1332 | probable phosphoes |
| 1377 | 62 | 5.2 | 273 | 2 | B70010 | potassium channel |
| 1378 | 62 | 5.2 | 287 | 2 | H95943 | dihydrolipoamide s |
| 1379 | 62 | 5.2 | 287 | 2 | A69838 | probable sugar upt |
| 1380 | 62 | 5.2 | 306 | 2 | A10209 | transcription regu |
| 1381 | 62 | 5.2 | 306 | 2 | T41290 | probable sugar ABC |
| 1382 | 62 | 5.2 | 312 | 2 | S48851 | conserved hypothet |
| 1383 | 62 | 5.2 | 312 | 2 | S48849 | cytochrome-c oxida |
| 1384 | 62 | 5.2 | 315 | 2 | T24821 | probable permease |
| 1385 | 62 | 5.2 | 331 | 2 | AB3117 | hypothetical prote |
| 1386 | 62 | 5.2 | 344 | 2 | N95987 | chalcone reductase |
| 1387 | 62 | 5.2 | 345 | 2 | T32203 | chalcone reductase |
| 1388 | 62 | 5.2 | 351 | 2 | C86408 | hypothetical prote |
| 1389 | 62 | 5.2 | 351 | 2 | C86170 | hypothetical prote |
| 1390 | 62 | 5.2 | 362 | 2 | S42379 | hypothetical prote |
| 1391 | 62 | 5.2 | 363 | 2 | B57641 | F3H9.12 protein - |
| 1392 | 62 | 5.2 | 370 | 2 | H84111 | hypothetical prote |
| 1393 | 62 | 5.2 | 377 | 2 | T05427 | response regulator |
| 1394 | 62 | 5.2 | 377 | 2 | H95943 | response regulator |
| 1395 | 62 | 5.2 | 379 | 2 | S58457 | hypothetical prote |
| 1396 | 62 | 5.2 | 381 | 1 | T11440 | hypothetical prote |
| 1397 | 62 | 5.2 | 383 | 2 | E58851 | bicyclomycin resis |
| 1398 | 62 | 5.2 | 383 | 2 | E64112 | hypothetical prote |
| 1399 | 62 | 5.2 | 393 | 2 | F72417 | ubiquinol-cytochro |
| 1400 | 62 | 5.2 | 399 | 2 | JC5279 | ubiquinol-cytochro |
| 1401 | 62 | 5.2 | 400 | 2 | C95965 | cell-division prot |
| 1402 | 62 | 5.2 | 402 | 2 | D70186 | translocation prot |
| 1403 | 62 | 5.2 | 403 | 2 | B69038 | hypothetical prote |
| 1404 | 62 | 5.2 | 411 | 2 | H72084 | xylose operon regu |
| 1405 | 62 | 5.2 | 432 | 1 | A34845 | conserved hypothet |
| 1406 | 62 | 5.2 | 432 | 2 | H72084 | cbs domain protein |
| 1407 | 62 | 5.2 | 432 | 2 | A34845 | protein-tyrosine-p |
| 1408 | 62 | 5.2 | 435 | 2 | T21880 | hypothetical prote |
| 1409 | 62 | 5.2 | 444 | 2 | T47737 | probable transmemb |
| 1410 | 62 | 5.2 | 454 | 2 | F81367 | probable transmemb |
| 1411 | 62 | 5.2 | | 2 | H65054 | hypothetical prote |

| ID | Score | | | Length | | Accession | Description |
|---|---|---|---|---|---|---|---|
| 1417 | 62 | 2 | 5.2 | 458 | 2 | A84487 | probable replicati |
| 1418 | 62 | 2 | 5.2 | 466 | 2 | AH1800 | transmembrane effl |
| 1419 | 62 | 2 | 5.2 | 474 | 2 | E64232 | hypothetical prote |
| 1420 | 62 | 2 | 5.2 | 483 | 2 | S46124 | nuclear protein EN |
| 1421 | 62 | 2 | 5.2 | 487 | 2 | T05271 | probable 3-oxoacyl |
| 1422 | 62 | 1 | 5.2 | 497 | 2 | T20799 | hypothetical prote |
| 1423 | 62 | 2 | 5.2 | 497 | 2 | S53834 | NADH2 dehydrogenas |
| 1424 | 62 | 2 | 5.2 | 499 | 2 | S66834 | probable membrane |
| 1425 | 62 | 2 | 5.2 | 502 | 2 | B81914 | probable periplasm |
| 1426 | 62 | 2 | 5.2 | 514 | 2 | AE23372 | probable membrane |
| 1427 | 62 | 1 | 5.2 | 528 | 2 | A96671 | hypothetical prote |
| 1428 | 62 | 2 | 5.2 | 555 | 2 | ACCH2N | nicotinic acetylch |
| 1429 | 62 | 2 | 5.2 | 567 | 2 | T08869 | protein P2 - Acryt |
| 1430 | 62 | 2 | 5.2 | 582 | 2 | S29498 | lymphocyte antigen |
| 1431 | 62 | 2 | 5.2 | 585 | 2 | S19424 | hypothetical prote |
| 1432 | 62 | 2 | 5.2 | 600 | 2 | T02360 | hypothetical prote |
| 1433 | 62 | 2 | 5.2 | 600 | 2 | H98149 | ATP-binding transp |
| 1434 | 62 | 2 | 5.2 | 630 | 2 | H83686 | hypothetical prote |
| 1435 | 62 | 2 | 5.2 | 644 | 2 | T20034 | PTS system, beta-g |
| 1436 | 62 | 2 | 5.2 | 660 | 2 | A44432 | hypothetical prote |
| 1437 | 62 | 2 | 5.2 | 667 | 1 | T20799 | amino acid transpo |
| 1438 | 62 | 2 | 5.2 | 675 | 1 | S46952 | hypothetical prote |
| 1439 | 62 | 2 | 5.2 | 678 | 2 | F71921 | phosphotransferase |
| 1440 | 62 | 2 | 5.2 | 702 | 2 | T20822 | hypothetical prote |
| 1441 | 62 | 2 | 5.2 | 707 | 2 | T03903 | nucleolin - human |
| 1442 | 62 | 2 | 5.2 | 724 | 1 | A35804 | heat shock protein |
| 1443 | 62 | 2 | 5.2 | 739 | 2 | HHMS84 | hypothetical prote |
| 1444 | 62 | 2 | 5.2 | 743 | 2 | A29232 | 101K malaria antig |
| 1445 | 62 | 2 | 5.2 | 750 | 2 | S73829 | probable ABC trans |
| 1446 | 62 | 1 | 5.2 | 756 | 2 | A88679 | protein H06H21.10 |
| 1447 | 62 | 2 | 5.2 | 791 | 2 | A46616 | cytochrome-c oxida |
| 1448 | 62 | 2 | 5.2 | 810 | 1 | A33380 | interleukin-4 rece |
| 1449 | 62 | 2 | 5.2 | 841 | 2 | T09455 | vacuolar assembly |
| 1450 | 62 | 2 | 5.2 | 848 | 2 | E95092 | aminopeptidase N | |
| 1451 | 62 | 2 | 5.2 | 864 | 2 | T42556 | tegument protein 1 |
| 1452 | 62 | 1 | 5.2 | 872 | 1 | TNBEEH | 97K alpha trans-in |
| 1453 | 62 | 2 | 5.2 | 911 | 2 | S70958 | otnA protein - Vib |
| 1454 | 62 | 2 | 5.2 | 932 | 2 | C70191 | penicillin-binding |
| 1455 | 62 | 2 | 5.2 | 950 | 1 | PWBYR1 | Ca2+-transporting |
| 1456 | 62 | 2 | 5.2 | 1002 | 2 | G97217 | conserved membrane |
| 1457 | 62 | 2 | 5.2 | 1024 | 1 | AE3557 | acriflavin resista |
| 1458 | 62 | 2 | 5.2 | 1030 | 2 | T13163 | Rab6 GTPase activa |
| 1459 | 62 | 2 | 5.2 | 1031 | 2 | T43458 | hypothetical prote |
| 1460 | 62 | 2 | 5.2 | 1041 | 2 | T29010 | hypothetical prote |
| 1461 | 62 | 2 | 5.2 | 1242 | 2 | G88480 | protein C16A3.7 [i |
| 1462 | 62 | 2 | 5.2 | 1273 | 2 | C96767 | unknown protein F2 |
| 1463 | 62 | 2 | 5.2 | 1283 | 2 | T18939 | hypothetical prote |
| 1464 | 62 | 2 | 5.2 | 1321 | 2 | A60165 | sodium channel pro |
| 1465 | 62 | 2 | 5.2 | 1780 | 2 | T20695 | hypothetical prote |
| 1466 | 62 | 2 | 5.2 | 1802 | 2 | T33783 | hypothetical prote |
| 1467 | 62 | 2 | 5.2 | 6359 | 2 | T31679 | bacitracin synthet |
| 1468 | 62 | 2 | 5.2 | 99 | 2 | B99233 | hypothetical prote |
| 1469 | 61.5 | 2 | 5.2 | 134 | 2 | E69985 | hypothetical prote |
| 1470 | 61.5 | 2 | 5.1 | 149 | 2 | C86655 | hypothetical prote |
| 1471 | 61.5 | 2 | 5.1 | 150 | 2 | S43955 | probable NADH2 deh |
| 1472 | 61.5 | 2 | 5.1 | 159 | 2 | S77185 | lipoprotein signal |
| 1473 | 61.5 | 2 | 5.1 | 162 | 2 | AF2618 | epithelial membran |
| 1474 | 61.5 | 2 | 5.1 | 162 | 2 | E97400 | hypothetical prote |
| 1475 | 61.5 | 2 | 5.1 | 163 | 2 | JC5045 | hypothetical prote |
| 1476 | 61.5 | 2 | 5.1 | 173 | 2 | H97775 | hypothetical prote |
| 1477 | 61.5 | 2 | 5.1 | 176 | 2 | G89947 | hypothetical prote |
| 1478 | 61.5 | 2 | 5.1 | 176 | 2 | S40726 | conserved hypothet |
| 1479 | 61.5 | 2 | 5.1 | 183 | 2 | H70478 | nucleoplasmin A - |
| 1480 | 61.5 | 2 | 5.1 | 185 | 2 | H69327 | conserved hypothet |
| 1481 | 61.5 | 2 | 5.1 | 190 | 2 | A26630 | hypothetical prote |
| 1482 | 61.5 | 2 | 5.1 | 212 | 2 | A83521 | hypothetical prote |
| 1483 | 61.5 | 2 | 5.1 | 225 | 2 | T19811 | hypothetical prote |
| 1484 | 61.5 | 2 | 5.1 | 225 | 2 | T19811 | hypothetical prote |
| 1485 | 61.5 | 2 | 5.1 | 264 | 2 | T18998 | hypothetical prote |
| 1486 | 61.5 | 2 | 5.1 | 272 | 2 | G82888 | hypothetical prote |
| 1487 | 61.5 | 2 | 5.1 | 273 | 2 | T28980 | NADH2 dehydrogenas |
| 1488 | 61.5 | 2 | 5.1 | 274 | 2 | S42168 | hypothetical prote |
| 1489 | 61.5 | 2 | 5.1 | 276 | 2 | F72342 | conserved hypothet |
| 1490 | 61.5 | 2 | 5.1 | 278 | 2 | D83080 | hypothetical prote |
| 1491 | 61.5 | 2 | 5.1 | 279 | 2 | AQ0421 | sugar transport sy |
| 1492 | 61.5 | 2 | 5.1 | 284 | 2 | AC3429 | perosamine synthet |
| 1493 | 61.5 | 2 | 5.1 | 289 | 2 | F91269 | hypothetical prote |
| 1494 | 61.5 | 2 | 5.1 | 289 | 2 | D86110 | hypothetical prote |
| 1495 | 61.5 | 2 | 5.1 | 290 | 2 | AE0947 | ribonuclease BN (E |
| 1496 | 61.5 | 2 | 5.1 | 292 | 2 | AE1539 | sugar ABC transpor |
| 1497 | 61.5 | 2 | 5.1 | 293 | 2 | C90032 | hypothetical prote |
| 1498 | 61.5 | 2 | 5.1 | 293 | 2 | A83710 | ABC transporter (p |
| 1499 | 61.5 | 2 | 5.1 | 293 | 2 | B69866 | transcription regu |
| 1500 | 61.5 | 2 | 5.1 | 294 | 2 | AD0886 | probable oxidoredu |

## ALIGNMENTS

RESULT 1
I38027
MLN 64 protein - human

C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: I38027; S60682
R;Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lidereau, R.
A;Title: Identification of four novel human genes amplified and overexpressed in breast
Genomics 28, 367-376, 1995
A;Reference number: I37080; MUID:96039245; PMID:7490069
A;Accession: I38027
A;Molecule type: mRNA
A;Residues: 1-445 <RES>
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: UNIPARC:UPI000012F1BC; EMBL:X80198; NID:g951278; PID
C;Genetics:
A;Gene: MLN64

Query Match 55.6%; Score 664; DB 2; Length 445;
Best Local Similarity 56.2%; Pred. No. 8.7e-55;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

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Qy    1 MNHLP-----EDMENALL---------TGSGQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV  51
           : |: | |:|:|         |||||||:|||||||||||||||:||||:|||:|||:|
Db    1 MSKLPRELTRDLERSLPAVASLGSSLSHSQSLSSHHLPPPE------------KRRAISDV  49

Qy   52 RRTFCLFVTFDLLFVTLLMIIELNVNGGIENTLEKEVMQYDYSSSYFDIFLLAVFRFKVL 111
          ||||||||||||||||||||: |||:||: :|:|:||||:|:|||||||||||| |||
Db   50 RRTFCLFVTFDLLFISILWIIELNTNTGIRKNLEQEIIQYNFKTSFFDIFVLAFFRFSGL 109

Qy  112 ILAYAVCRLRHWWAIALITTAVTSAFLLAKYVIISKLFSQGAFGYVLPIISFILAWIETWFL 171
          :|||::|| ||: ||:||:||||:|||:|||||:|||||:: |:|||:||||||:|||| |||
Db  110 LLGYAVLQLRHWWVIAVTTLVSSAFLIVKRITLSEELLSKGAFGYLLPIVSFVLAWLETWFL 169

Qy  172 DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEEKQDSEK 229
          |||||||||||||: |||:||||||:||:||||||||||||||:||||| ||| |||:||
Db  170 DFKVLPQEAEERWYLAAQVAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVAGKK 229
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RESULT 2
T16170
hypothetical protein F26F4.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16170
R;Fulton, L.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F26F4.
A;Reference number: Z18471
A;Accession: T16170
A;Molecule type: DNA
A;Residues: 1-478 <FUL>
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: UNIPARC:UPI000017B938; EMBL:U12964; NID:g1213452; PI
C;Genetics:
A;Experimental source: strain Bristol N2

A;Gene: CESP:F26F4.4
A;Introns: 47/2; 81/2; 125/3; 171/3; 214/2; 236/2; 343/3; 444/1

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Qy   Query Match
     Best Local Similarity  17.1%;        Score 204;  DB 2;  Length 478;
     Matches  56;  Conservative  36;  Mismatches  73;  Indels  46;  Gaps  6;

Qy     42  GREKKGISDVRRTFCLFVTFDLLFVTLLWII--------ELNVNGGIENTLEK  86
               |:| :||| | :|| |||  ||:|||||        ||::|| |||||||
Db     69  GSQRIGVSKDRKRFIVITFPDTISITILLWLLCTVVTRDDDWDKVFFNEINI------FNP 121

Qy     87  EVMQYDYYSSYFDIFLLAVFRKFKVLILAYAVCRLRHWWAIALITAVTSAFLLAKVILSKL 146
               :|| |||||||||||||||||||||||||||||||||||||||| |:|| :|
Db    122  KFIRI----SLFDIVLLAVRMLLIGVVVGICLVKQWYTVAFTTLASSAYILMKVLFYEN  177

Qy    147  FSQGAFGYVLPII-SFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSD  205
               |  |  |:|  | ||| |||   |||| :::    |: |     ::||  |  |:
Db    178  HSSSAVPLLLIITSFTLCWSEFYLMPFQILPRERYARREL------------DGIEN  224

Qy    206  GQFYSPPESEA-----------GSEEAEEKQDSEKP 230
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Db    225  PEFSTDDEARSNNRHRRGRRQQNSGNQSEAP 255
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RESULT 3
H90281
hypothetical protein dppB-1 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90281
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.;
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
R;She, Q.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90281
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <KUR>
A;Genetics: UNIPROT:Q97YQ0; UNIPARC:UPI0000064305; GB:AE006641; NID:g13814471; F
A;Gene: dppB-1

```
Qy   Query Match
     Best Local Similarity  23.7%;        Score 102.5;  DB 2;  Length 348;
     Matches  49;  Conservative  35;  Mismatches  66;  Indels  57;  Gaps  9;

Qy     15  SQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLFVTLLWIIEL  74
               ||||| ||| ||| |  || :  |||||||||||||| |||||||||| | |
Db     46  AQFSQTLFKNAHNLNSTQIQIAVEKY--RE----------------------SLIAAYGL  81

Qy     75  NVNGGIENTLEK---------EVMQYDYYSSYFDIFLLAVFRKFKVLILAYAVCRLRHWWAIAL  128
               :  |||||||          ||| |||||||||||||||||||||||
Db     82  N------QPIIDKYFIQMYNLMRFDFGTAYF-LQAPSGSREVSSIIAYYLPN-----TILL  130

Qy    129  TTAVTSAFLLAKVILSKLFSQGAF-GYVLPIISFILAWIETWFLDFKVLPQEAEEENRLL  187
               ||||||||||||| |||    |  ||:|  |||| ||||   ||||   :|
Db    131  FTTATVFIVAGTIIGLLSAKSKFWEKVIAIIAVHSSIPTWWLGF----------------VL  178

Qy    188  IVQDASERAALIPGGLSDGQFYSPPES  214
               ||       |: |   | ||:|
Db    179  IAALAYAVKVFPPGGMTS---VPPPKN  202
```

RESULT 4
D75080
glucose-1-phosphate thymidylyltransferase related protein PAB2433 - Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
R;anonymous,
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence; insights into archaeal chromosome stru.
A;Reference number: A75001
A;Accession: D75080
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-424 <KAW>
A;Cross-references: UNIPROT:Q9UZW1; UNIPARC:UPI00000347IC; GB:AJ248286; GB:AL096836; NID
A;Experimental source: strain Orsay
A;Gene: PAB2433
C;Genetics:
C;Superfamily: Aquifex aeolicus glucose-1-phosphate thymidylyltransferase

```
Qy   Query Match
     Best Local Similarity  7.8%;         Score 93.5;  DB 2;  Length 424;
     Matches  47;  Conservative  25;  Mismatches  72;  Indels  71;  Gaps  7;

Qy      5  PEDMENA------------------------------LTGSQSSHASLRNIHSINPTQLMARIESYEGRE  44
               |||||                         | |||||||||||||||||||||
Db    207  PEDIKKARKLIVTISVKGVGDGFISRHLNRKISTRISALLVEHVTPNQM-----------  255

Qy     45  KKGISDVRRTFCLFVTFDL-LFVTLLWIIELNVNG------GIENTLEKEVMQYDY  93
               ||||||||||||||||||  |||||| |||:  ||        |: |:||||:||
Db    256  --------TIVTFLFGIFSALMNFSVPIAGILYQVSSILDGVDGEIARARMQTSK  303

Qy     94  YSSYFDIFLLAVFRFK-VLILAYAVCRLRHWWAIALITAVTSAFL----------------L 138
               ||||||||||||||   ||||| ||||||||||||||| | ||||
Db    304  FGGYFPDSILDRYVDFTFLILAYVSIREPLWWAIAIAMFSSAMYSYSTERFKGAYCVDA 363

Qy    139  AKVI--LSKLFSQGAFGYVLPIISFILAWIETWFL 171
               |||:   |  ||||| |||| | ||| |||||||
Db    364  YKVIPALRKVPGKRDERIFLTMLLTLVGWIKALFL 398
```

RESULT 5
T43048
calcium channel alpha-1 chain - Cyanea capillata
C;Species: Cyanea capillata
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
R;Jeziorski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V.
J. Biol. Chem. 273, 22792-22799, 1998
R;Jeziorski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V.
A;Title: Cloning and functional expression of a voltage-gated calcium channel alphal sub
A;Reference number: Z22300; MUID:98380510; PMID:9712913
A;Accession: T43048
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1911 <JEZ>
A;Cross-references: UNIPROT:O02038; UNIPARC:UPI00000070488; EMBL:U93075; NID:g1947095; PI
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein

```
Qy   Query Match
     Best Local Similarity  7.5%;         Score 90;  DB 2;  Length 1911;
     Matches  43;  Conservative  33;  Mismatches  59;  Indels  48;  Gaps  9;

Qy      5  PEDMENALTGSQSSHASLRNIHSINPTQLM----ARIESYEGREKKGISDV  51
               |||:|||  |    |||||||||||||| |    ||||||||||||||||
Db    791  PEDVE--LGNPKSKNGTLRHMGETTSTEMSEGKEARIRPLRLSEUNLLKDIPDPMPPESS 848

Qy     52  -----RRTFCLFVTFDLLFVT--LLMIIELNVNGGIENTLEKEVMQYDYYSSYFDI 100
                    ||||||||||||| |  | ||:|||||:| |||:|| | || |||||||
Db    849  FFIFSANNKLRYLCYRLAVNKIFINSILVLIIMSSVALAAEDPIGRDVLR-NKILGYFDI 907

Qy    101  FLLAVFRFKVLI--LAYAV-------------CR------------LRHWWAIAILTT-AVTAAFLLA 139
               ||||||||||:   |||||             ||            |||||||| | |||: |||:
Db    908  FFTAMPFEVTVKRMIAFGVILHKRSFCRSFFNQLDLVIVAVSWAAIMLSRGSATSVRIL 967

Qy    140  KVI 142
               |:|
Db    968  RVL 970
```

RESULT 6

T21969
hypothetical protein F38E11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
A;Accession: T21969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Accession: T21969
R;Matthews, P.
submitted to the EMBL Data Library, January 1996
A;Reference number: Z19495
A;Accession: T21969
A;Molecule type: DNA
A;Residues: 1-767 <WIL>
A;Cross-references: UNIPARC:UPI0000074B2B; EMBL:Z68342; PIDN:CAA92775.1;
.; E.M.; de Vos, N.; van Ommen, G.J.B.; Breuning, M.H.; Doggett, N.A.; Meincke, L.J.; Liu,
A;Cross-references: UNIPROT:Q20170;
A;Genetics:
C;Genetics:
A;Gene: CESP:F38E11.7
A;Map position: 4
A;Experimental source: clone F38E11
A;Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1; 6

Best Local Similarity   24.8%;   Pred. No. 5.3;
Matches  35; Conservative  22; Mismatches  49; Indels  35; Gaps   5;

Qy     61 FDLLFVTLLWIIELNVNGGIIENTLEKEVMQYDYSSYFDIFILLAVFRFKVLIL---AYAV 117
             |  |:|    :|  : |    |  :|||| |||||||:| ||||||:|||      | |
Db    109 FDIILRSMLSFYE----DGVLITSFSETWRHYVHSFYFADLLAIFPFDYLLIRKTSAAF 164

Qy    118 CRLRHWW------------AIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPI 158
              || |              | | ::||:||  ||: ||| |:| |: || :|
Db    165 CRLNRFLKIYRIANFIAQSYGKLTQVTISLSKIFTACFLLFHV------NACVFYIISV 217

Qy    159 ISFILAW--IETWFLDFKVLP 177
             |||| |   || |:|| ||
Db    218 NSDTSSWDGVNATFDDDEYLP 238

Best Local Similarity   24.8%; ...

RESULT 7
B81299
probable molybdopterin biosynthesis protein Cj1519 [imported] - Campylobacter jejuni (st
C;Species: Campylobacter jejuni
A;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C;Accession: B81299
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: B81299
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <PAR>
A;Cross-references: UNIPARC:UPI00000C1F59; GB:AL139078; GB:AL111168; NID
C;Genetics:
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: moeA2; Cj1519
C;Superfamily: molybdenum cofactor molybdenum incorporation protein MoeA

Query Match        7.2%;    Score 85.5;  DB 2;  Length 396;
Best Local Similarity   21.0%;   Pred. No. 3;
Matches  47; Conservative  35; Mismatches  81; Indels  61; Gaps   9;

Qy      4 LPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLF----- 58
            | :|||| :|  |:   |  : ||| : |  |||:  :| | :|| | |:|:|
Db    185 LGEALENPAQIRSSNHIAIANL----------------AKNLNCDRVFPLLKDDEK 225

Qy     59 VTFDLLFVTLLWIIELNVNGGIE---NTLEKEVMQYDYSSYFDI------------- 100
            |:|||||| :|  :| ||| |    ||||| |||||||||:|
Db    226 ATFSTLESALQSCDILVTTGGVSMGDFDFLKKAIKEYEIIDKADIKPGRHIKIAKANEK 285

Qy    101 FLLAV--FRFKVLLLAYAVCR--LRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVL 156
            ||| |  ||||: | |      |||| : || :||:||  ||: ||| |:| |:|| :|
Db    286 FIIALPGFFYSAMVMFNLYTREILNSW--------------LLQPKDYICKAFLQSSYKKKT 333

Qy     (continued columns)

RESULT 8
A57219
Batten disease-related protein CLN3 - human
C;Species: Homo sapiens (man)
A;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C;Accession: A57219
A;Accession: A57219
R;Lerner, T.J.; Boustany, R.M.N.; Anderson, J.W.; D'Arigo, K.L.; Schlumpf, K.; Buckler,
.; Mole, S.E.
Cell 82, 949-957, 1995
A;Title: Isolation of a novel gene underlying Batten disease, CLN3.
A;Reference number: A57219; MUID:96016090; PMID:7553855
A;Accession: A57219
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Map position: 16p12.1-16p11.2
A;Cross-references: UNIPROT:Q13286; UNIPARC:UPI000000000ED; GB:U32680; NID:g1039422; PIDN
C;Genetics:
A;Gene: GDB:CLN3
A;Cross-references: GDB:120593; OMIM:204200
C;Superfamily: CLN3 protein/Battenin (Batten disease protein)
C;Keywords: membrane protein

Query Match        7.2%;    Score 85.5;  DB 2;  Length 438;
Best Local Similarity   25.5%;   Pred. No. 3.4;
Matches  38; Conservative  18; Mismatches  46; Indels  47; Gaps   8;

Qy     64 LFVTLLWII------------ENTLEKEVMQYDYSSYFDIFILLAVFRF 108
            ||:|| |:             ||||| |||||||||:| ||||||:||
Db    277 VFKGLLWYIVPLVVVYFAEYFINQGLFELLFFWNTSLSHAQQYRWYQM---LYQAGVFAS 333

Qy    109 KVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFIL---- 163
            ||:| |     |||| : || :||:||  ||: ||| |:| |:|| :||||||:|
Db    334 R---SSLRCCRIRFTWALALLQCLNLVFLLADV-----WFGF-LPSIYLVFLILY 380

Qy    164 ------AWIETWFLDFKVLPQEAEEENR 185
                  | :| |:|||||| |:| |  |
Db    381 EGLLGGAAYVNT---FHNIALETSDEHR 405

Qy    157 PIISFILAWIETWFLDFKVLPQ-EAEEENRLLIVQDASERALI 199
            | ::| || :| |:|||||| |  | ||| |::| |: :| |
Db    334 PYLEFVACNIE--FKNGRILANLEGKKEGSSAIINNLNNKAALM 375

RESULT 9
G70172
conserved hypothetical integral membrane protein BB0584 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
A;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70172
A;Accession: G70172
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70172
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-448 <KLE>
A;Cross-references: UNIPROT:O51531; UNIPARC:UPI000005752F; GB:AE001160; GB:AE000783; NID
A;Experimental source: strain B31

Query Match        7.1%;    Score 85;  DB 2;  Length 448;
Best Local Similarity   24.4%;   Pred. No. 3.9;
Matches  47; Conservative  28; Mismatches  64; Indels  54; Gaps  11;

Qy     50 DVRRTFCLFVTFDLLFVTL---IWIIELNVNGGIE-NTLEKEVMQYDYSS------Y 97
            ||:| |  |:|:|||||||    |:|||| |||:  ||||| |||||||||
Db    271 DTHKYAAYSISFSIYFIIFNIIHSFCISLNIMMGYEMHNSKKEIMKVAIYLSKIGLKLAF 330

```
Qy   98 FDIFLLAVRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVI--LSKLFSQGA---- 151
           | :|  ||: ||  | |  |||:|| | ||  |||| :  |   |||||||
Db  331 LTSFVLPIFSFPAPYIFYTL-KYSHLIGILRYSSVSAFFMALAPQYLFGFPRAGASPSF 389

Qy  152 ------FGYVLPIISFILAWIETWFLDFKVLPQEAEEENRLLIV------QDASERAA 197
              :|| ||:|  |||:     ||          : ||  |||
Db  390 GAIMEGSVFFVYTIP-IAFVLA----------NYTNLPFE------IIVFIPSLEDAIKLVV 434

Qy  198 LIPGGLSDGQFYS 210
           :|         ||
Db  435 SLP------YFYS 441
```

RESULT 10
A41680
integral membrane protein pssA - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1992
R;Kuge, O.; Nishijima, M.; Akamatsu, Y.
J. Biol. Chem. 266, 24184-24189, 1991
A;Title: A Chinese hamster cDNA encoding a protein essential for phosphatidylserine synt
A;Reference number: A41680; MUID:9208472; PMID:1748667
A;Accession: A41680
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-471 <KUG>
A;Cross-references: UNIPARC:UPI000012280F; GB:D10234; GB:D90468; NID:g220280; PIDN:BAA01
A;Superfamily: membrane protein
C;Keywords: membrane protein

Query Match 7.1%; Score 84.5; DB 2; Length 471;
Best Local Similarity 24.4%; Pred. No. 4.6;
Matches 32; Conservative 22; Mismatches 38; Indels 39; Gaps 7;

```
Qy   55 FCLFVTFDLLFVTLLMIIELNVNGGIENTLEKEVMQY----------DYYSSYFDIFLLAV 105
          | : | ||: |: :   ||| |    :   |  ||          :|| |||||| ||
Db  117 FLLFLNFEQVKSLMYW-LDPNLRYA--TREADIMEYANVNCHVITWERIVSHFDIFAFGH 172

Qy  106 F---RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISF 161
          |    ||  |  | |  | |      |||| :   | |           ||:|  ||:
Db  173 FWGNAMKALLIRSYGLC-----WITSITWELTELF------------FMHLLP-NF 210

Qy  162 ILAWIETWFLD 172
          |  |     |
Db  211 AECWWDQVILD 221
```

RESULT 11
H97002
probable integral membrane protein [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97002
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Makarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <KUR>
A;Cross-references: UNIPROT:Q97KT1; UNIPARC:UPI0000000CFCF; GB:AE001437; PIDN:AAK78811.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
A;Genetics:
A;Gene: CAC0835

Query Match 7.0%; Score 83.5; DB 2; Length 352;
Best Local Similarity 19.2%; Pred. No. 4.1;
Matches 38; Conservative 35; Mismatches 50; Indels 75; Gaps 8;

```
Qy   38 ESYEGREKKGISDVRRTFCLFVTFD-------------------------LLFVTLLMIIEL 74
            | :    ||   |  ||||                                 ||:|||||||
Db  115 EFYNVRDKKTNEDMKKLIKAYLVQNKTLNMERIVKDEQIGGLSKSERIIAFLATVLLITS 174

Qy   75 NVNGGI------ENTLEKEVMQ------------YDYYSSYFDIF-----LLAVRFKVL 111
          :|||          | :         |         |||||||||      ||||||||
Db  175 VVNGAVIIRDREENTYYRIMYSPNSKFEYIFGNVIYNYIFSYIQLFIANSLMAIFGIYIG 234

Qy  112 I-----LAYAVCRLRHWWAIALTTAVTSAF-------LLAKVILSKLFSQGAFGYVLPIIS 160
          |     | || |  | |  ||||||||||        :  | |||||||||| || ||
Db  235 ISFLKMLSYGL----------ILTLVMTFGTFIVCIFNKELYANMFSAA-------IS 276

Qy  161 FILAWIETWFLDFKVLPQ 178
          :||:|      | | :|
Db  277 LILSLVGGTFINYKIMPE 294
```

RESULT 12
AE0302
sugar ABC transporter, permease protein YPO2476 [imported] - Yersinia pestis (strain CO9
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0302
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0302
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-291 <KUR>
A;Cross-references: UNIPROT:Q8ZDT0; UNIPARC:UPI00000DCC19; GB:AL590842; PIDN:CAC91281.1;
C;Genetics:
A;Gene: YPO2476
C;Superfamily: inner membrane protein

Query Match 6.9%; Score 83; DB 2; Length 291;
Best Local Similarity 22.3%; Pred. No. 3.6;
Matches 44; Conservative 26; Mismatches 57; Indels 70; Gaps 10;

```
Qy    9 KQVGSVLAASYLGIYSIFWPYFIWLAVSLTEWRFVGIPTFNGLNNFILVWMQDPLFWKS 68
          |:  ||  |:|| |  :|    ||||| ||||| ||:         |     |||
Db   85 EKEVMQYDYSSYFDIFLLAVRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKV-- 141

Qy   69 MLNVWRFLMY--YLPIVFISSFLF-----AFGLQKLKHG----RTFVALSFLLANVSSG 116
          :|       :   |||  |:| ||     |||           ||  || |||
Db  142 ------ILSKLFSQGA------FGYVLPIIS----FILAWIETW-------FL 171

Qy  117 VAYSIVFSKLFSQNGPLNTFLYDWFGFTLPWLTSPDFAMLSIALVVTWKFVGYYGLILFS 176
          | : |  |||||||:||| |||:| | |||:||||| ||||||| |:  |||| |||||
Db  172 DFKVLPQE---AEEEN 184

Qy  177 GLNSIPKEIYSAAELDN 193
Db  177 GLNSIPKEIYSAAELDN 193
```

RESULT 13
S34960
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti mitochondrio
C;Species: mitochondrion Crithidia oncopelti
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S34960
R;Maslov, D.A.; Horvath, A.; Gwang II, K.; Kolesnikov, A.A.
submitted to the EMBL Data Library, October 1990
A;Reference number: S34958
A;Accession: S34960
A;Molecule type: DNA
A;Residues: 1-590 <MAS>
A;Cross-references: UNIPROT:O34192; UNIPARC:UPI000008E400; EMBL:X56015; NID:g12879; PIDN
C;Genetics:

A;Gene: ND5
A;Genome: mitochondrion
A;Genetic code: SGC6
A;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
A;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

```
Query Match             6.9%;   Score 83;  DB 1;   Length 590;
Best Local Similarity  23.9%;   Pred. No. 8.3;
Matches   32;  Conservative  23;  Mismatches  37;  Indels  42;  Gaps  7;

Qy   55 FCLFVTF-----DLL--FVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVF 106
           |||:   :|| :::|  :   :
Db   95 FILFYAFYIMYYDLMLKRFFNIFWMFVLCMMFFI------LSYDYLTAYCGWELLGLF 146

Qy  107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWI 166
           |||| | ::|   :||   |  ::||:|    :::|
Db  147 SF--FLISY---FWYRFFALKFGFKSFFISKI----------GDVLLLLSFVMTFI 187

Qy  167 ET-------WFLDF 173
                   :|::|:
Db  188 STGYGMINFYFVNF 201
```

RESULT 14
B29835
TraS protein - Escherichia coli plasmid pED208
C;Species: Escherichia coli
C;Date: 04-Aug-1988 #sequence_revision 04-Aug-1988 #text_change 09-Jul-2004
C;Accession: B29835
R;Finlay, B.B.; Paranchych, W.
J;Bacteriol. 166, 713-721, 1986
A;Title: Nucleotide sequence of the surface exclusion genes traS and traT from the IncF-
A;Accession: B29835
A;Reference number: A29835; MUID:8622783; PMID:3011738
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <FIN>
A;Cross-references: UNIPROT:P14498; UNIPARC:UPI000001563
A;Genome: plasmid

```
Query Match             6.9%;   Score 82.5;  DB 2;   Length 186;
Best Local Similarity  23.8%;   Pred. No. 2.4;
Matches   31;  Conservative  24;  Mismatches  40;  Indels  35;  Gaps  6;

Qy   61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLL------AVFRFKVLILAY 115
           |:||| |    |  |::          :|::  |
Db   44 FQLLFI----IFDIFINSNVR------DYH--YFDTFVITLGSNAFFSLVFLMSTY 87

Qy  116 AVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPII----------SFILAW 165
           | | :      | ::||:   |:  |::           :|: |
Db   88 NLVSLK----ISLGSEITEQSVLLKLVERKINSYGQFLMVVNAIVGCVLLSSGERFVAGL 143
```

RESULT 15
C64227
hypothetical protein homolog MG247 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: C64227
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: C64227
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-239 <TIGR>
A;Cross-references: UNIPROT:P47489; UNIPARC:UPI0000001394F7; GB:U39703; GB:L43967; NID:g3E
A;Experimental source: strain G-37
A;Genetics:
A;Genetic code: SGC3
A;Superfamily: Escherichia coli ygiH protein

```
Query Match             6.9%;   Score 82.5;  DB 1;   Length 239;
Best Local Similarity  21.7%;   Pred. No. 3.2;
Matches   33;  Conservative  26;  Mismatches  54;  Indels  39;  Gaps  8;

Qy   42 GREKKGISDVRRTF-----------CLFVTFDLLFVTLL-WIIELNVNGGIENTLEKEVMQYD 92
           | ::        |:|          :||| |   |  :
Db   42 GSKNPGATNSMRVFGLKIGFLVAIFDDAFKGFFAFLLTWIL---FRFGLQGYLTEKYVQST 98

Qy   93 YYSSYFDIFLLAV-------FRFK----VLILAYAVCRLRHWWAI------ALTTAVTSA 135
           |::|           ||:|     ||  | | :       | ::
Db   99 YFLSYLSCFAATIGHIFFPLYFKPKGGKAIATTGGSLLAISLMWFLICLLIWIMITLITKY 158

Qy  136 FLLAKVILSKLFSQGAFGYVLPIISFILAWIE 167
           |:| ||         :|::  |::
Db  159 VSLASLITF----------FVLAVI-ILIPWLD 180
```

Search completed: October 31, 2006, 02:26:22
Job time : 75 secs

OM protein - protein search, using sw model

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GenCore version 5.1.9

Run on:    October 31, 2006, 02:25:39 ; Search time 301 Seconds
           (without alignments)
           719.115 Million cell updates/sec

Title:         US-10-063-518-14
Perfect score: 1195
Sequence:      1 MNHLPEDMENALTGSQSSHA.........EAGSEEAEEKQDSEKPLLEL 234

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
Searched:      2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters:    2849598
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries
Database :     UniProt 7.2.*
               1:  uniprot_sprot.*
               2:  uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES.

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1195 | 100.0 | 234 | 1 | MENTO_HUMAN | O95772 homo sapien |
| 2 | 1141.5 | 95.5 | 235 | 1 | Q5U205_RAT | Q5U205 rattus norv |
| 3 | 1134.5 | 94.9 | 235 | 1 | MENTO_MOUSE | Q9DC13 mus musculu |
| 4 | 1134.5 | 94.9 | 235 | 1 | Q3U807_MOUSE | Q3U8Q7 mus musculu |
| 5 | 1128.5 | 94.4 | 235 | 2 | Q3U852_MOUSE | Q3U852 mus musculu |
| 6 | 796 | 66.6 | 227 | 2 | Q6DI38_BRARE | Q6DI38 brachydanio |
| 7 | 700.5 | 58.6 | 448 | 2 | Q6DFR7_XENTR | Q6DFR7 xenopus tro |
| 8 | 699.5 | 58.5 | 444 | 2 | Q6PF40_XENLA | Q6PF40 xenopus lae |
| 9 | 684 | 57.2 | 444 | 2 | Q6GNT3_XENLA | Q6GNT3 xenopus lae |
| 10 | 664 | 55.6 | 448 | 1 | O14849_HUMAN | O14849 homo sapien |
| 11 | 664 | 55.6 | 445 | 1 | Q53Y53_HUMAN | Q53Y53 homo sapien |
| 12 | 656.5 | 54.9 | 446 | 2 | Q61542_MOUSE | Q61542 mus musculu |
| 13 | 656.5 | 54.9 | 446 | 2 | MLN64_MOUSE | mus musculu |
| 14 | 656.5 | 54.9 | 446 | 2 | Q54C3_MOUSE | Q54C3 mus musculu |
| 15 | 656.5 | 54.9 | 446 | 1 | Q5U2T5_RAT | Q5U2T5 rattus norv |
| 16 | 632 | 52.9 | 448 | 2 | MLN64_BRARE | Q9DF84 brachydanio |
| 17 | 586.5 | 49.1 | 444 | 2 | Q4S943_TETNG | Q4S943 tetraodon n |
| 18 | 566 | 47.4 | 501 | 2 | Q5RB70_PONPY | Q5RB70 pongo pygma |
| 19 | 566 | 47.4 | 574 | 2 | Q56D1_AEDAE | Q56D1 aedes aegyp |
| 20 | 364.5 | 30.5 | 595 | 2 | Q56300_AEDAE | Q56300 aedes aegyp |
| 21 | 364.5 | 30.5 | 523 | 2 | Q7QIT3_ANOGA | Q7QIT3 anopheles g |
| 22 | 343 | 28.7 | 545 | 2 | Q8MZH4_DROME | Q8MZH4 drosophila |
| 23 | 343 | 28.7 | 583 | 1 | Q9W145_DROME | Q9W145 drosophila |
| 24 | 342.5 | 28.7 | 131 | 2 | Q4TH5_TETNG | Q4TH5 tetraodon n |
| 25 | 330 | 27.6 | 476 | 2 | Q3V5Y6_BOMMO | Q3V5Y6 bombyx mori |
| 26 | 272 | 22.8 | 197 | 2 | Q4SN2_TETNG | Q4SN2 tetraodon n |
| 27 | 209.5 | 17.5 | 185 | 2 | Q5BVU9_SCHJA | Q5BVU9 schistosoma |
| 28 | 206.5 | 17.3 | 419 | 2 | Q60270_CAEBR | Q60270 caenorhabdi |
| 29 | 204 | 17.1 | 447 | 2 | Q19819_CAEEL | Q19819 caenorhabdi |
| 30 | 181.5 | 15.2 | 141 | 2 | Q4SNJ3_TETNG | Q4SNJ3 tetraodon n |
| 31 | 117 | 9.8 | 459 | 2 | Q46F23_METBA | Q46F23 methanosarc |
| 32 | 104.5 | 8.7 | 294 | 1 | MLN64_SALFO | salvelinus |
| 33 | 102.5 | 8.6 | 348 | 2 | Q97YQ0_SULSO | Q97YQ0 sulfolobus |
| 34 | 100.5 | 8.4 | 369 | 2 | Q31ET4_THICR | Q31ET4 thiomicrosp |
| 35 | 99.5 | 8.3 | 1095 | 2 | Q4N7C1_THEPA | Q4N7C1 theileria p |
| 36 | 96.5 | 8.1 | 714 | 2 | Q5LPT4_SILPO | Q5LPT4 silicibacte |
| 37 | 95.5 | 8.0 | 493 | 2 | Q37IK3_RHOPA | Q37IK3 rhodopseudo |
| 38 | 93.5 | 7.9 | 616 | 2 | Q30SK2_THIDN | Q30SK2 thiomicrosp |
| 39 | 93.5 | 7.8 | 424 | 2 | Q9UZW1_PYRAB | Q9UZW1 pyrococcus |
| 40 | 93.5 | 7.8 | 564 | 1 | CLN3_MACFA | macaca fasc |
| 41 | 92.5 | 7.7 | 304 | 2 | Q60HH0_THRIM | Q60HH0 thrips imag |
| 42 | 92 | 7.7 | 246 | 2 | Q8HQ10_THRIM | Q8HQ10 thrips imag |
| 43 | 91 | 7.6 | 525 | 2 | Q21X08_RHOPA | Q21X08 rhodopseudo |
| 44 | 91 | 7.6 | 651 | 2 | Q3D2J8_STRAG | Q3D2J8 streptococc |
| 45 | 91 | 7.6 | 651 | 2 | Q3D8X6_STRAG | Q3D8X6 streptococc |
| 46 | 91 | 7.6 | 651 | 2 | Q7VFT4_HELHP | Q7VFT4 helicobacte |
| 47 | 91 | 7.6 | 651 | 2 | Q8DU10_STRMU | Q8DU10 streptococc |
| 48 | 91 | 7.6 | 262 | 2 | Q3DUY5_STRAG | Q3DUY5 streptococc |
| 49 | 91 | 7.6 | 284 | 2 | Q3K1B2_STRA1 | Q3K1B2 streptococc |
| 50 | 90.5 | 7.6 | 530 | 2 | Q8DZX0_STRA5 | Q8DZX0 streptococc |
| 51 | 90.5 | 7.6 | 401 | 2 | Q8E5M0_STRA3 | Q8E5M0 streptococc |
| 52 | 90.5 | 7.6 | 262 | 2 | Q7NBJ4_MYCGA | Q7NBJ4 mycoplasma |
| 53 | 90 | 7.5 | 284 | 2 | Q3WYL1_9ACTN | Q3WYL1 rubrobacter |
| 54 | 90 | 7.5 | 401 | 2 | Q54F03_DICDI | Q54F03 dictyosteli |
| 55 | 89.5 | 7.5 | 233 | 2 | Q36VR4_RHOPA | Q36VR4 rhodopseudo |
| 56 | 89.5 | 7.5 | 1911 | 2 | Q02038_CYACP | Q02038 cyanea capi |
| 57 | 89.5 | 7.5 | 233 | 2 | Q6JCT3_9HEMI | Q6JCT3 aleurodicus |
| 58 | 89.5 | 7.5 | 376 | 2 | Q8HEH8_9ACAR | Q8HEH8 varroa dest |
| 59 | 89.5 | 7.5 | 478 | 2 | Q6JCT6_9HEMI | Q6JCT6 aleurodicus |
| 60 | 89.5 | 7.5 | 488 | 2 | Q840W7_STRMU | Q840W7 streptococc |
| 61 | 89 | 7.4 | 373 | 2 | Q7RTB5_PLAYO | Q7RTB5 plasmodium |
| 62 | 89 | 7.4 | 387 | 2 | Q568R5_BRARE | Q568R5 brachydanio |
| 63 | 89 | 7.4 | 651 | 2 | Q3DLX9_STRAG | Q3DLX9 streptococc |
| 64 | 89 | 7.4 | 897 | 2 | Q5K830_CRYNE | Q5K830 cryptococc |
| 65 | 88.5 | 7.4 | 912 | 2 | Q4YCI1_PLABE | Q4YCI1 plasmodium |
| 66 | 88 | 7.4 | 384 | 2 | Q6WN4_RANCA | Q6WN4 rana cates |
| 67 | 88 | 7.4 | 453 | 2 | Q4C173_CROWT | Q4C173 crocosphaer |
| 68 | 87.5 | 7.3 | 755 | 2 | Q60QU6_CAEBR | Q60QU6 caenorhabdi |
| 69 | 87.5 | 7.3 | 396 | 2 | Q4HDY8_CAMCO | Q4HDY8 campylobact |
| 70 | 87 | 7.3 | 473 | 2 | Q5ZM65_CHICK | Q5ZM65 gallus gall |
| 71 | 87 | 7.3 | 301 | 2 | Q3KQH5_XENLA | Q3KQH5 xenopus lae |
| 72 | 87 | 7.3 | 304 | 2 | Q640E5_XENLA | Q640E5 xenopus lae |
| 73 | 87 | 7.3 | 610 | 2 | Q7RRS2_PLAYO | Q7RRS2 plasmodium |
| 74 | 87 | 7.2 | 707 | 2 | Q6GN42_XENLA | Q6GN42 xenopus lae |
| 75 | 87 | 7.2 | 720 | 2 | Q8PYM2_METWA | Q8PYM2 methanosarc |
| 76 | 86 | 7.2 | 756 | 2 | Q55IJ0_CRYNE | Q55IJ0 cryptococc |
| 77 | 86 | 7.2 | 328 | 2 | Q55IJ9_GLOVI | Q55IJ9 gloeobacter |
| 78 | 86.5 | 7.2 | 626 | 2 | Q7NLJ9_GLOVI | Q7NLJ9 gloeobacter |
| 79 | 86.5 | 7.2 | 647 | 2 | Q7Z2O5_CAEEL | Q7Z2O5 caenorhabdi |
| 80 | 86.5 | 7.2 | 891 | 2 | Q8JLA2_9POXV | Q8JLA2 plasmodium |
| 81 | 86 | 7.2 | 613 | 2 | Q2RIX6_MOOTH | Q2RIX6 moorella th |
| 82 | 86 | 7.2 | 1050 | 2 | Q871G6_NEUCR | Q871G6 neurospora |
| 83 | 86 | 7.2 | 1056 | 2 | Q7S7L6_NEUCR | Q7S7L6 neurospora |
| 84 | 86 | 7.2 | 1453 | 2 | Q4PAR7_USTMA | Q4PAR7 ustilago ma |
| 85 | 86 | 7.2 | 2515 | 2 | Q4S220_TETNG | Q4S220 tetraodon n |
| 86 | 86 | 7.2 | 174 | 2 | P97067_9ENTR | P97067 salmonella |
| 87 | 85 | 7.2 | 336 | 2 | Q2UP48_ASPOR | Q2UP48 aspergillus |
| 88 | 85 | 7.1 | 337 | 2 | Q95086_HUMAN | Q95086 homo sapien |
| 89 | 85 | 7.1 | 337 | 2 | Q4Y634_PLACH | Q4Y634 plasmodium |
| 90 | 85 | 7.1 | 339 | 2 | Q95089_HUMAN | Q95089 homo sapien |
| 91 | 85 | 7.1 | 360 | 2 | Q2TA70_HUMAN | Q2TA70 homo sapien |
| 92 | 85 | 7.1 | 396 | 2 | Q9PME5_CAMJE | Q9PME5 campylobact |
| 93 | 85 | 7.2 | 438 | 1 | CLN3_HUMAN | homo sapien |
| 94 | 85 | 7.2 | 451 | 2 | Q47H59_DECAR | Q47H59 dechloromon |
| 95 | 85 | 7.2 | 473 | 1 | PTSS1_HUMAN | homo sapien |
| 96 | 85 | 7.2 | 473 | 2 | Q93GL8_SALTY | Q93GL8 salmonella |
| 97 | 85 | 7.2 | 747 | 2 | Q2KHY9_BOVIN | Q2KHY9 bos taurus |
| 98 | 85 | 7.1 | 302 | 2 | Q9SF17_ARATH | Q9SF17 arabidopsis |
| 99 | 85 | 7.1 | 448 | 2 | Q612C1_BACAN | Q612C1 bacillus an |
| 100 | 85 | 7.1 | 377 | 2 | Q615S1_BORBU | Q615S1 borrelia bu |
| 101 | 85 | 7.1 | 448 | 2 | Q82GJ8_STRAW | Q82GJ8 streptomyce |
| 102 | 85 | 7.1 | 797 | 2 | Q4B5Q6_9BURK | Q4B5Q6 polaromonas |
| 103 | 84.5 | 7.1 | 2793 | 2 | Q4ITL6_AZOVI | Q4ITL6 azotobacter |
| 104 | 84.5 | 7.1 | 412 | 2 | | |

**Block 1 (entries 105–177)**

| No. | % | E | Len | N | Accession | Organism |
|---|---|---|---|---|---|---|
| 105 | 84.5 | 7.1 | 430 | 2 | Q5ZTB7_LEGPH | q5ztb7 legionella |
| 106 | 84.5 | 7.1 | 471 | 1 | PTSS1_CRIGR | ptss1 cricetulus |
| 107 | 84.5 | 7.1 | 473 | 1 | Q99LH2 | q99lh2 mus muscul |
| 108 | 84.5 | 7.1 | 473 | 2 | Q3UV14_MOUSE | q3uv14 mus muscul |
| 109 | 84.5 | 7.1 | 473 | 2 | Q5PQL5_RAT | q5pql5 rattus norv |
| 110 | 84.5 | 7.1 | 487 | 2 | Q6A0E5_MOUSE | q6a0e5 mus muscul |
| 111 | 84.5 | 7.1 | 620 | 2 | Q3Q9T9_9GAMM | q3q9t9 shewanella |
| 112 | 84.5 | 7.1 | 886 | 2 | Q2RAN1_ORYSA | q2ran1 oryza sativ |
| 113 | 84.5 | 7.1 | 892 | 2 | Q9JF90_VACCT | q9jf90 vaccinia vi |
| 114 | 84.5 | 7.1 | 895 | 2 | Q2TWS5_ASPOR | q2tws5 aspergillus |
| 115 | 84.5 | 7.1 | 1118 | 2 | Q6SU88_MANSM | q6su88 mannheimia |
| 116 | 84.5 | 7.1 | 3848 | 2 | Q5CUX5_CRYPV | q5cux5 cryptospori |
| 117 | 84.5 | 7.1 | 396 | 2 | Q5HSR1_CAMJR | q5hsr1 campylobact |
| 118 | 84 | 7.0 | 468 | 2 | Q42828_DESHA | q42828 desulfitoba |
| 119 | 84 | 7.0 | 469 | 2 | Q9HJK8_THEAC | q9hjk8 thermoplasm |
| 120 | 84 | 7.0 | 493 | 2 | Q7TSH7_MOUSE | q7tsh7 m potassium |
| 121 | 84 | 7.0 | 809 | 2 | Q43RP5_SOLUS | q43rp5 solibacter |
| 122 | 84 | 7.0 | 1700 | 2 | Q75JN1_DICDI | q75jn1 dictyosteli |
| 123 | 83.5 | 7.0 | 170 | 2 | Q4YS32_PLABE | q4ys32 plasmodium |
| 124 | 83.5 | 7.0 | 275 | 2 | Q8XIT3_CLOPE | q8xit3 clostridium |
| 125 | 83.5 | 7.0 | 276 | 2 | Q4D766_TRYCR | q4d766 trypanosoma |
| 126 | 83.5 | 7.0 | 303 | 2 | Q6FNB8_CANGA | q6fnb8 candida gla |
| 127 | 83.5 | 7.0 | 322 | 2 | Q8LB40_ARATH | q8lb40 arabidopsis |
| 128 | 83.5 | 7.0 | 352 | 2 | Q97KK1_CLOAB | q97kk1 clostridium |
| 129 | 83.5 | 7.0 | 355 | 2 | Q6K124_MYCMO | q6k124 mycoplasma |
| 130 | 83.5 | 7.0 | 380 | 2 | Q97C55_THEVO | q97c55 thermoplasm |
| 131 | 83.5 | 7.0 | 429 | 2 | Q5E5F1_VIBF1 | q5e5f1 vibrio fisc |
| 132 | 83.5 | 7.0 | 490 | 2 | Q9CTA9_MOUSE | q9cta9 mus muscul |
| 133 | 83.5 | 7.0 | 503 | 2 | Q36S46_MARHY | q36s46 marinobacte |
| 134 | 83.5 | 7.0 | 599 | 2 | Q6PCX2_MOUSE | q6pcx2 mus muscul |
| 135 | 83.5 | 7.0 | 662 | 2 | Q88P20_PSEPK | q88p20 pseudomonas |
| 136 | 83.5 | 7.0 | 834 | 2 | Q9JHF5_MOUSE | q9jhf5 mus muscul |
| 137 | 83.5 | 7.0 | 834 | 2 | Q9JL12_MOUSE | q9jl12 mus muscul |
| 138 | 83.5 | 7.0 | 834 | 2 | Q91W06_MOUSE | q91w06 mus muscul |
| 139 | 83.5 | 7.0 | 1034 | 2 | Q72ZB9_TRYCR | q72zb9 trypanosoma |
| 140 | 83.5 | 7.0 | 2483 | 2 | Q5CH29_CRYHO | q5ch29 cryptospori |
| 141 | 83 | 7.0 | 238 | 2 | Q6YR96_ONYPE | q6yr96 onion yello |
| 142 | 83 | 7.0 | 248 | 2 | Q8GC56_EUBAC | q8gc56 eubacterium |
| 143 | 83 | 7.0 | 280 | 2 | Q3JED6_NITOC | q3jed6 nitrosococc |
| 144 | 83 | 7.0 | 291 | 2 | Q8ZDT0_YERPE | q8zdt0 yersinia pe |
| 145 | 83 | 7.0 | 438 | 2 | Q5XIH8_RAT | q5xih8 rattus norv |
| 146 | 83 | 7.0 | 589 | 2 | Q7TMW1_MOUSE | q7tmw1 mus muscul |
| 147 | 83 | 7.0 | 590 | 2 | Q34192_CRION | q34192 crithidia o |
| 148 | 83 | 7.0 | 738 | 2 | Q30S24_THIDN | q30s24 thiomicrosp |
| 149 | 83 | 7.0 | 1056 | 2 | Q8C2V1_MOUSE | q8c2v1 mus muscul |
| 150 | 83 | 6.9 | 1388 | 2 | Q5DU28_MOUSE | q5du28 mus muscul |
| 151 | 83 | 6.9 | 2661 | 2 | Q7RMS4_PLAYO | q7rms4 plasmodium |
| 152 | 82.5 | 6.9 | 174 | 1 | P97231_9ENTR | p97231 salmonella |
| 153 | 82.5 | 6.9 | 186 | 1 | TRAS2_ECOLI | tras2 escherichia |
| 154 | 82.5 | 6.9 | 186 | 2 | Q7BBW2_SALTI | q7bbw2 salmonella |
| 155 | 82.5 | 6.9 | 218 | 2 | Q3IQR1_NATPD | q3iqr1 natronomona |
| 156 | 82.5 | 6.9 | 239 | 1 | Y247_MYCGE | y247 mycoplasma |
| 157 | 82.5 | 6.9 | 255 | 2 | Q36E00_9GAMM | q36e00 shewanella |
| 158 | 82.5 | 6.9 | 341 | 2 | Q56918_YEREN | q56918 yersinia en |
| 159 | 82.5 | 6.9 | 367 | 2 | Q8HCX3_9ACAR | q8hcx3 varroa dest |
| 160 | 82.5 | 6.9 | 389 | 2 | Q5FL80_LACAC | q5fl80 lactobacill |
| 161 | 82.5 | 6.9 | 406 | 2 | O87249_9LACT | o87249 lactococcus |
| 162 | 82.5 | 6.9 | 419 | 2 | O19134_RABIT | o19134 oryctolagus |
| 163 | 82.5 | 6.9 | 422 | 2 | Q333G1_9CAUD | q333g1 bacteriopha |
| 164 | 82.5 | 6.9 | 471 | 2 | Q95OM6_9FUNG | q95om6 rhizophydiu |
| 165 | 82.5 | 6.9 | 510 | 2 | Q9QW77_CRIGR | q9qw77 cricetulus |
| 166 | 82.5 | 6.9 | 604 | 2 | Q8RHJ3_FUSNN | q8rhj3 fusobacteri |
| 167 | 82.5 | 6.9 | 717 | 2 | TRAD1_ECOLI | trad1 escherichia |
| 168 | 82.5 | 6.9 | 781 | 2 | Q4U8E8_THEAN | q4u8e8 theileria a |
| 169 | 82.5 | 6.9 | 891 | 2 | Q49PU1_9POXV | q49pu1 vaccinia vi |
| 170 | 82.5 | 6.9 | 891 | 2 | Q6J3A9_9POXV | q6j3a9 vaccinia vi |
| 171 | 82.5 | 6.9 | 891 | 2 | Q80DW2_COWPX | q80dw2 cowpox viru |
| 172 | 82.5 | 6.9 | 891 | 2 | Q6RZH3_9POXV | q6rzh3 rabbitpox v |
| 173 | 82.5 | 6.9 | 892 | 2 | Q8QMU0_COWPX | q8qmu0 cowpox viru |
| 174 | 82.5 | 6.9 | 894 | 2 | Q80QM0_COWPX | q80qm0 cowpox viru |
| 175 | 82.5 | 6.9 | 1022 | 2 | Q88VO0_LACPL | q88vo0 lactobacill |
| 176 | 82 | 6.9 | 156 | 2 | Q81501_9HEPC | q81501 hepatitis c |
| 177 | 82 | 6.9 | 161 | 2 | O69UD2_ORYSA | o69ud2 oryza sativ |

**Block 2 (entries 178–250)**

| No. | % | E | Len | N | Accession | Organism |
|---|---|---|---|---|---|---|
| 178 | 82 | 6.9 | 201 | 2 | Q6COH8_YARLI | q6coh8 yarrowia li |
| 179 | 82 | 6.9 | 228 | 2 | RGP1_MOUSE | rgp1 mus musculu |
| 180 | 82 | 6.9 | 301 | 2 | Q6NZB5_MOUSE | q6nzb5 mus musculu |
| 181 | 82 | 6.9 | 303 | 2 | Q89L18_BRAJA | q89l18 bradyrhizob |
| 182 | 82 | 6.9 | 316 | 2 | Q61RL6_CAEBR | q61rl6 caenorhabdi |
| 183 | 82 | 6.9 | 382 | 2 | Q6ZPH4_MOUSE | q6zph4 mus musculu |
| 184 | 82 | 6.9 | 384 | 2 | Q50HU1_PORGI | q50hu1 porphyromon |
| 185 | 82 | 6.9 | 387 | 2 | Q30PJ9_THIDN | q30pj9 thiomicrosp |
| 186 | 82 | 6.9 | 461 | 2 | Q6AHB8_LEIXX | q6ahb8 leifsonia x |
| 187 | 82 | 6.9 | 472 | 2 | Q70J50_HAEIN | q70j50 haemophilus |
| 188 | 82 | 6.9 | 564 | 2 | Q2UHP4_ASPOR | q2uhp4 aspergillus |
| 189 | 82 | 6.9 | 581 | 2 | Q4RQN5_TETNG | q4rqn5 tetraodon n |
| 190 | 82 | 6.9 | 587 | 2 | P46061_MOUSE | p46061 mus musculu |
| 191 | 82 | 6.9 | 589 | 2 | Q6NZB5_MOUSE | q6nzb5 m rangapl p |
| 192 | 82 | 6.9 | 589 | 2 | Q8C2E3_MOUSE | q8c2e3 mus musculu |
| 193 | 82 | 6.9 | 589 | 2 | Q91Y82_MOUSE | q91y82 mus musculu |
| 194 | 82 | 6.9 | 589 | 2 | Q6ZPH4_MOUSE | q6zph4 mus musculu |
| 195 | 82 | 6.9 | 646 | 2 | Q8PXU3_METMA | q8pxu3 methanosarc |
| 196 | 82 | 6.9 | 647 | 2 | Q4HJJ3_CAMLA | q4hjj3 campylobact |
| 197 | 82 | 6.9 | 819 | 2 | Q4JCD0_SULAC | q4jcd0 sulfolobus |
| 198 | 82 | 6.9 | 819 | 2 | Q6CDE6_YARLI | q6cde6 yarrowia li |
| 199 | 82 | 6.9 | 989 | 2 | Q81564_PLAF7 | q81564 yarrowia li |
| 200 | 82 | 6.9 | 989 | 2 | P78576_EMENI | p78576 emericella |
| 201 | 82 | 6.9 | 1031 | 1 | Q5AS02_EMENI | q5as02 aspergillus |
| 202 | 82 | 6.9 | 1466 | 2 | Q9KIA9_ENTHI | q9kia9 escherichia |
| 203 | 82 | 6.9 | 1466 | 2 | Q51D23_ENTHI | q51d23 entamoeba h |
| 204 | 81.5 | 6.9 | 190 | 2 | Q9B893_9TREM | q9b893 schistosoma |
| 205 | 81.5 | 6.9 | 283 | 2 | Q2X2A4_SHEPU | q2x2a4 shewanella |
| 206 | 81.5 | 6.9 | 297 | 2 | Q2XSH6_MOUSE | q2xsh6 mus musculu |
| 207 | 81.5 | 6.9 | 306 | 2 | Q8CDI4_MOUSE | q8cdi4 mus musculu |
| 208 | 81.5 | 6.9 | 306 | 2 | Q22083_9GAMM | q22083 uncultured |
| 209 | 81.5 | 6.8 | 311 | 2 | RNFD_PASMU | rnfd pasteurella |
| 210 | 81.5 | 6.8 | 342 | 1 | Q9H7E5_HUMAN | q9h7e5 homo sapien |
| 211 | 81.5 | 6.8 | 349 | 1 | Q72CJ7_DESVH | q72cj7 homo sapien |
| 212 | 81.5 | 6.8 | 352 | 2 | Q4VBD2_MOUSE | q4vbd2 desulfovibr |
| 213 | 81.5 | 6.8 | 387 | 2 | Q6PAH4_MOUSE | q6pah4 mus musculu |
| 214 | 81.5 | 6.8 | 391 | 2 | Q35934_MOUSE | q35934 mus musculu |
| 215 | 81.5 | 6.8 | 414 | 2 | Q8C5B1_MOUSE | q8c5b1 blochmannia |
| 216 | 81.5 | 6.8 | 438 | 2 | Q7VRC0_BLOFL | q7vrc0 listeria mo |
| 217 | 81.5 | 6.8 | 447 | 2 | Q4EJ15_LISMO | q4ej15 brachydanio |
| 218 | 81.5 | 6.8 | 463 | 2 | O80309_BRARE | o80309 homo sapien |
| 219 | 81.5 | 6.8 | 465 | 2 | Q9NVS8_HUMAN | q9nvs8 homo sapien |
| 220 | 81.5 | 6.8 | 519 | 2 | Q6P126_HUMAN | q6p126 homo sapien |
| 221 | 81.5 | 6.8 | 519 | 2 | O7Z748_HUMAN | o7z748 homo sapien |
| 222 | 81.5 | 6.8 | 577 | 2 | O67UQ9_ORYSA | o67uq9 oryza sativ |
| 223 | 81.5 | 6.8 | 577 | 2 | Q8DLB4_SYNEL | q8dlb4 synechococc |
| 224 | 81.5 | 6.8 | 645 | 2 | Q8B3YG_ECOLI | q8b3yg escherichia |
| 225 | 81.5 | 6.8 | 716 | 2 | Q775R6_CAMPS | q775r6 escherichia |
| 226 | 81.5 | 6.8 | 735 | 2 | Q8VZP5_ASHGO | q8vzp5 salmonella |
| 227 | 81.5 | 6.8 | 892 | 2 | Q75SK6_ASHGO | q75sk6 ashbya goss |
| 228 | 81.5 | 6.8 | 892 | 1 | Q4SGQ6_TETNG | q4sgq6 natronomona |
| 229 | 81.5 | 6.8 | 1092 | 2 | Q7R386_GIALA | q7r386 shewanella |
| 230 | 81.5 | 6.8 | 1472 | 2 | Q5KGP3_CRYNE | q5kgp3 yersinia en |
| 231 | 81.5 | 6.8 | 1480 | 2 | Q55S96_CRYNE | q55s96 varroa dest |
| 232 | 81.5 | 6.8 | 1659 | 2 | Q2NFQ6_9EURY | q2nfq6 lactobacill |
| 233 | 81.5 | 6.8 | 1692 | 2 | Q2KY24_BORAV | q2ky24 lactococcus |
| 234 | 81.5 | 6.8 | 216 | 2 | Q9Z6G9_ARATH | q9z6g9 oryctolagus |
| 235 | 81.5 | 6.8 | 285 | 2 | Q4MPN6_BACCE | q4mpn6 arabidopsis |
| 236 | 81 | 6.8 | 385 | 2 | Q6D043_ERWCT | q6d043 bordetella |
| 237 | 81 | 6.8 | 410 | 2 | Q63E77_BACCZ | q63e77 methanospha |
| 238 | 81 | 6.8 | 483 | 2 | Q63ET7_BACCZ | q63et7 giardia lam |
| 239 | 81 | 6.8 | 486 | 2 | Q5AL74_CANAL | q5al74 cryptococcu |
| 240 | 81 | 6.8 | 492 | 2 | Q5A405_CANAL | q5a405 cryptococcu |
| 241 | 81 | 6.8 | 510 | 1 | YOUL_CAEEL | youl candida alb |
| 242 | 81 | 6.8 | 520 | 1 | YHB7_YEAST | yhb7 saccharomyc |
| 243 | 81 | 6.8 | 532 | 2 | Q3H702_TRIER | q3h702 trichodesmi |
| 244 | 81 | 6.8 | 780 | 2 | Q8XSV5_RALSO | q8xsv5 ralstonia s |
| 245 | 81 | 6.8 | 805 | 2 | Q8QRL8_9HEPC | q8qrl8 hepatitis c |
| 246 | 81 | 6.8 | 3010 | 2 | P97066_9ENTR | p97066 salmonella |
| 247 | 80.5 | 6.7 | 174 | 2 | Q2NIM4_9MOLU | q2nim4 aster yello |
| 248 | 80.5 | 6.7 | 240 | 2 | Q8TNE9_METAC | q8tne9 methanococc |
| 249 | 80.5 | 6.7 | 242 | 2 | Q3PSH1_NITHA | q3psh1 nitrobacter |
| 250 | 80.5 | 6.7 | 284 | 2 | Q56WV6_ARATH | q56wv6 arabidopsis |

**Block 3 (far-right column — accession / organism)**

| Accession | Organism |
|---|---|
| Q45PY3_9CAUD | bacteriopha |
| Q5ESD8_VIBF1 | vibrio fisc |
| Q8RLZ3_HAEIN | haemophilus |
| Q89L18_BRAJA | bradyrhizob |
| Q61RL6_CAEBR | caenorhabdi |
| Q3H702_TRIER | trichodesmi |
| Q8C2E3_MOUSE | mus musculu |
| Q91Y82_MOUSE | mus musculu |
| Q8PXU3_METMA | methanosarc |
| Q4HJJ3_CAMLA | campylobact |
| Q4JCD0_SULAC | sulfolobus |
| Q6CDE6_YARLI | yarrowia li |
| Q81564_PLAF7 | plasmodium |
| P78576_EMENI | emericella |
| Q5AS02_EMENI | aspergillus |
| Q9KIA9_9ENTR | escherichia |
| Q51D23_ENTHI | entamoeba h |
| Q9B893_9TREM | schistosoma |
| Q2X2A4_SHEPU | shewanella |
| Q2XSH6_MOUSE | mus musculu |
| Q22083_9GAMM | uncultured |
| Q9H7E5_HUMAN | pasteurella |
| Q72CJ7_DESVH | homo sapien |
| Q4VBD2_MOUSE | homo sapien |
| Q6PAH4_MOUSE | desulfovibr |
| Q35934_MOUSE | mus musculu |
| Q8C5B1_MOUSE | mus musculu |
| Q7VRC0_BLOFL | blochmannia |
| Q4EJ15_LISMO | listeria mo |
| O80309_BRARE | brachydanio |
| Q9NVS8_HUMAN | homo sapien |
| Q6P126_HUMAN | homo sapien |
| O7Z748_HUMAN | homo sapien |
| O67UQ9_ORYSA | homo sapien |
| Q8DLB4_SYNEL | oryza sativ |
| Q8B3YG_ECOLI | synechococc |
| Q775R6_CAMPS | escherichia |
| Q8VZP5_ASHGO | escherichia |
| Q75SK6_ASHGO | salmonella |
| Q4SGQ6_TETNG | ashbya goss |
| Q7R386_GIALA | natronomona |
| Q5KGP3_CRYNE | shewanella |
| Q55S96_CRYNE | yersinia en |
| Q2NFQ6_9EURY | varroa dest |
| Q2KY24_BORAV | lactobacill |
| Q9Z6G9_ARATH | lactococcus |
| Q4MPN6_BACCE | oryctolagus |
| Q6D043_ERWCT | arabidopsis |
| Q63E77_BACCZ | bordetella |
| Q63ET7_BACCZ | methanospha |
| Q5AL74_CANAL | giardia lam |
| Q5A405_CANAL | cryptococcu |
| YOUL_CAEEL | cryptococcu |
| YHB7_YEAST | saccharomyc |
| Q3H702_TRIER | trichodesmi |
| Q8XSV5_RALSO | ralstonia s |
| Q8QRL8_9HEPC | hepatitis c |
| P97066_9ENTR | salmonella |
| Q2NIM4_9MOLU | aster yello |
| Q8TNE9_METAC | methanococc |
| Q3PSH1_NITHA | nitrobacter |
| Q56WV6_ARATH | arabidopsis |

| No | % | % | Len | Ct | Accession | Description |
|----|----|----|-----|----|-----------|-------------|
| 251 | 80.5 | 6.7 | 322 | 2 | Q9SNE5_ARATH | q9sne5 arabidopsis |
| 252 | 80.5 | 6.7 | 353 | 1 | P49217_PHOSU | p49217 phodopus su |
| 253 | 80.5 | 6.7 | 366 | 1 | Q86KR8_DICDI | q86kr8 dictyosteli |
| 254 | 80.5 | 6.7 | 396 | 1 | BIN1_SCHPO | bin1_schpo schizosacch |
| 255 | 80.5 | 6.7 | 417 | 1 | TNAB_PROVU | tnab_provu proteus vul |
| 256 | 80.5 | 6.7 | 423 | 2 | P28785 | p28785 streptococc |
| 257 | 80.5 | 6.7 | 463 | 2 | Q4K188_STRPN | q4k188 streptococc |
| 258 | 80 | 6.7 | 463 | 2 | Q72Q04_LISMO | q72q04 listeria mo |
| 259 | 80.5 | 6.7 | 463 | 2 | Q8Y988_LISMO | q8y988 listeria mo |
| 260 | 80.5 | 6.7 | 485 | 2 | Q5EAZ3_XENLA | q5eaz3 xenopus lae |
| 261 | 80.5 | 6.7 | 485 | 1 | Q54Z56_DICDI | q54z56 dictyosteli |
| 262 | 80.5 | 6.7 | 486 | 2 | Q9G861_9EUKA | q9g861 malawimonas |
| 263 | 80.5 | 6.7 | 536 | 1 | MVIN_CHLTR | mvin_chltr chlamydia t |
| 264 | 80.5 | 6.7 | 536 | 1 | Q3KL71_CHLTA | q3kl71 chlamydia t |
| 265 | 80.5 | 6.7 | 548 | 2 | Q7RC45_PLAYO | q7rc45 plasmodium |
| 266 | 80.5 | 6.7 | 554 | 1 | Q4Y6E4_PLACH | q4y6e4 plasmodium |
| 267 | 80.5 | 6.7 | 599 | 2 | Q91ME6_9REOV | q91me6 human rotav |
| 268 | 80.5 | 6.7 | 644 | 1 | P53925_YEAST | p53925 saccharomyc |
| 269 | 80.5 | 6.7 | 716 | 2 | Q6B2V3_ECOLI | q6b2v3 escherichia |
| 270 | 80.5 | 6.7 | 732 | 2 | Q2TU08_ECOLI | q2tu08 escherichia |
| 271 | 80.5 | 6.7 | 733 | 2 | Q6SIZ5_ECOLI | q6siz5 escherichia |
| 272 | 80.5 | 6.7 | 733 | 1 | Q3YTF2_SHISS | q3ytf2 shigella so |
| 273 | 80.5 | 6.7 | 738 | 2 | TRAD2_ECOLI | trad2_ecoli escherichia |
| 274 | 80.5 | 6.7 | 738 | 2 | Q7AK62_9ZZZZ | q7ak62 plasmid r10 |
| 275 | 80.5 | 6.7 | 784 | 2 | P22708_ECOLI | p22708 escherichia |
| 276 | 80.5 | 6.7 | 891 | 1 | Q7YWX2_CAEEL | q7ywx2 caenorhabdi |
| 277 | 80.5 | 6.7 | 891 | 1 | Q5IXQ4_MONPV | q5ixq4 monkeypox v |
| 278 | 80.5 | 6.7 | 891 | 2 | Q76ZQ5_9POXV | q76zq5 vaccinia vi |
| 279 | 80.5 | 6.7 | 891 | 1 | Q8V4W5_MONPV | q8v4w5 monkeypox v |
| 280 | 80.5 | 6.7 | 955 | 1 | Q2UU23_ASPOR | q2uu23 aspergillus |
| 281 | 80.5 | 6.7 | 1687 | 2 | Q7SC49_NEUCR | q7sc49 neurospora |
| 282 | 80.5 | 6.7 | 1780 | 2 | Q9ZT82_ARATH | q9zt82 arabidopsis |
| 283 | 80.5 | 6.7 | 103 | 1 | Q9RX39_DEIRA | q9rx39 deinococcus |
| 284 | 80.5 | 6.7 | 156 | 1 | 081513_9HEPC | 081513 hepatitis c |
| 285 | 80.5 | 6.7 | 197 | 1 | Q5QTD8_HUMAN | q5qtd8 homo sapien |
| 286 | 80 | 6.7 | 238 | 2 | Q95KH1_MACFA | q95kh1 macaca fasc |
| 287 | 80 | 6.7 | 238 | 2 | Q6V7H6_EAV | q6v7h6 equine arte |
| 288 | 80 | 6.7 | 255 | 2 | Q4MTK3_BACCE | q4mtk3 bacillus ce |
| 289 | 80 | 6.7 | 280 | 2 | Q635R8_BACCZ | q635r8 bacillus ce |
| 290 | 80 | 6.7 | 280 | 2 | Q6HEF5_BACHK | q6hef5 bacillus th |
| 291 | 80 | 6.7 | 280 | 2 | 0819H0_BACCR | 0819h0 bacillus ce |
| 292 | 80 | 6.7 | 280 | 2 | Q731V3_BACC1 | q731v3 bacillus ce |
| 293 | 80 | 6.7 | 280 | 2 | 081MM0_BACAN | 081mm0 bacillus an |
| 294 | 80 | 6.7 | 290 | 2 | Q7A5Y6_STAAN | q7a5y6 staphylococ |
| 295 | 80 | 6.7 | 290 | 2 | Q99UM2_STAAM | q99um2 staphylococ |
| 296 | 80 | 6.7 | 296 | 2 | Q3EEG9_ACTSC | q3eeg9 actinobacil |
| 297 | 80 | 6.7 | 300 | 2 | Q9C840_ARATH | q9c840 arabidopsis |
| 298 | 80 | 6.7 | 309 | 1 | RTM1_YEAST | rtm1_yeast saccharomyc |
| 299 | 80 | 6.7 | 343 | 2 | Q7USB9_RHOBA | q7usb9 rhodopirell |
| 300 | 80 | 6.7 | 347 | 2 | Q9FFM1_ARATH | q9ffm1 arabidopsis |
| 301 | 80 | 6.7 | 355 | 2 | Q73JA5_TREDE | q73ja5 treponema d |
| 302 | 80 | 6.7 | 359 | 2 | Q7N4F8_PHOLL | q7n4f8 photorhabdu |
| 303 | 80 | 6.7 | 360 | 2 | Q9H1X3_HUMAN | q9h1x3 homo sapien |
| 304 | 80 | 6.7 | 388 | 2 | Q58427_PYRHO | q58427 pyrococcus |
| 305 | 80 | 6.7 | 418 | 2 | Q3P007_9GAMM | q3p007 shewanella |
| 306 | 80 | 6.7 | 488 | 2 | Q65088_ORYSA | q65088 oryza sativ |
| 307 | 80 | 6.7 | 540 | 2 | Q6FX17_CANGA | q6fx17 candida gla |
| 308 | 80 | 6.7 | 554 | 2 | Q69FF8_ANOGA | q69ff8 anopheles ga |
| 309 | 80 | 6.7 | 650 | 2 | Q75SY6_ASHGO | q75sy6 ashbya goss |
| 310 | 80 | 6.7 | 661 | 2 | Q7VH08_HELIP | q7vh08 helicobacte |
| 311 | 80 | 6.7 | 680 | 2 | Q4EKL7_LISMO | q4ekl7 listeria mo |
| 312 | 80 | 6.7 | 700 | 2 | Q72OZ1_LISMF | q72oz1 listeria mo |
| 313 | 80 | 6.7 | 893 | 2 | Q4I7J8_GIBZE | q4i7j8 gibberella |
| 314 | 80 | 6.7 | 3010 | 2 | Q9QIY9_9HEPC | q9qiy9 hepatitis c |
| 315 | 80 | 6.7 | 360 | 2 | Q3SLE7_THIDA | q3sle7 thiobacillu |
| 316 | 80 | 6.7 | 266 | 2 | Q5IPF9_9RODE | q5ipf9 perognathus |
| 317 | 79.5 | 6.7 | 266 | 2 | Q5IPF8_9RODE | q5ipf8 perognathus |
| 318 | 79.5 | 6.7 | 266 | 2 | Q4EFC5_LISMO | q4efc5 listeria mo |
| 319 | 79.5 | 6.7 | 269 | 2 | Q72BD0_LISMF | q72bd0 listeria mo |
| 320 | 79.5 | 6.7 | 269 | 2 | Q3WS44_9RHIZ | q3ws44 mesorhizobi |
| 321 | 79.5 | 6.7 | 269 | 2 | Q33ZM2_RHOPA | q33zm2 rhodopseudo |
| 322 | 79.5 | 6.7 | 273 | 2 | | |
| 323 | 79.5 | 6.7 | 304 | 2 | | |

| No | % | % | Len | Ct | Accession | Description |
|----|----|----|-----|----|-----------|-------------|
| 324 | 79.5 | 6.7 | 307 | 2 | Q89NC2_BRAJA | q89nc2 bradyrhizob |
| 325 | 79.5 | 6.7 | 367 | 2 | Q8ESY3_OCEIH | q8esy3 oceanobacil |
| 326 | 79.5 | 6.7 | 379 | 2 | Q508J9_9RODE | q508j9 perognathus |
| 327 | 79.5 | 6.7 | 391 | 2 | Q6TY96_9BILA | q6ty96 xiphinema a |
| 328 | 79.5 | 6.7 | 392 | 2 | Q2MDL9_VIVIN | q2mdl9 viverricula |
| 329 | 79.5 | 6.7 | 404 | 2 | Q405X5_9RHOB | q405x5 jannaschia |
| 330 | 79.5 | 6.7 | 438 | 1 | CLN3_CANFA | cln3_canfa canis famil |
| 331 | 79.5 | 6.7 | 463 | 2 | Q92E11_LISIN | q92e11 listeria in |
| 332 | 79.5 | 6.7 | 468 | 2 | Q30R92_THIDN | q30r92 thiomicrosp |
| 333 | 79.5 | 6.7 | 488 | 2 | Q6QU70_ASPNG | q6qu70 aspergillus |
| 334 | 79.5 | 6.7 | 491 | 1 | VIE1_HCMVT | vie1_hcmvt human cytom |
| 335 | 79.5 | 6.7 | 546 | 1 | P60815_RAT | p60815 rattus norv |
| 336 | 79.5 | 6.7 | 598 | 2 | P03169_... | p03169 human cytom |
| 337 | 79.5 | 6.7 | 649 | 2 | Q42ZF3_PLABE | q42zf3 plasmodium |
| 338 | 79.5 | 6.7 | 674 | 2 | Q51954_BORHE | q51954 borrelia he |
| 339 | 79.5 | 6.7 | 688 | 2 | O86P19_DEBHA | o86p19 debaryomyce |
| 340 | 79.5 | 6.7 | 688 | 2 | Q6BZ08_DROME | q6bz08 drosophila |
| 341 | 79.5 | 6.7 | 726 | 2 | Q35Y20_9GAMM | q35y20 drosophila |
| 342 | 79.5 | 6.7 | 732 | 2 | Q22578_9GAMM | q22578 shewanella |
| 343 | 79.5 | 6.7 | 748 | 2 | Q9EUJ3_SALTI | q9euj3 salmonella |
| 344 | 79.5 | 6.7 | 784 | 2 | Q5J497_SALCH | q5j497 salmonella |
| 345 | 79.5 | 6.7 | 784 | 2 | Q9EUJ3_SALET | q9euj3 salmonella |
| 346 | 79.5 | 6.7 | 818 | 2 | Q4WB47_ASPFU | q4wb47 aspergillus |
| 347 | 79.5 | 6.7 | 886 | 2 | Q9VYY0_DROME | q9vyy0 drosophila |
| 348 | 79.5 | 6.7 | 1708 | 2 | Q8KDB0_CHLTE | q8kdb0 chlorobium |
| 349 | 79.5 | 6.6 | 3409 | 2 | Q5HXC6_CAMJR | q5hxc6 campylobact |
| 350 | 79 | 6.6 | 114 | 2 | Q4ALC7_9CHLB | q4alc7 chlorobium |
| 351 | 79 | 6.6 | 238 | 2 | Q4LE27_HUMAN | q4le27 homo sapien |
| 352 | 79 | 6.6 | 251 | 2 | Q7SI27_NEUCR | q7si27 neurospora |
| 353 | 79 | 6.6 | 288 | 2 | Q6VRR6_HELPY | q6vrr6 helicobacte |
| 354 | 79 | 6.6 | 288 | 2 | Q3UWH0_MOUSE | q3uwh0 mouse |
| 355 | 79 | 6.6 | 308 | 2 | Q6M0I2_METMP | q6m0i2 methanococc |
| 356 | 79 | 6.6 | 308 | 2 | Q3EEL5_ACTSC | q3eel5 actinobacil |
| 357 | 79 | 6.6 | 312 | 2 | O8O2H3_9MURI | o8o2h3 arvicanthis |
| 358 | 79 | 6.6 | 323 | 2 | O8RGM6_FUSNN | o8rgm6 fusobacteri |
| 359 | 79 | 6.6 | 345 | 2 | Q6KH29_MYCMO | q6kh29 mycoplasma |
| 360 | 79 | 6.6 | 349 | 1 | Q7KSI9_DROME | q7ksi9 drosophila |
| 361 | 79 | 6.6 | 350 | 2 | Q360Y1_9GAMM | q360y1 shewanella |
| 362 | 79 | 6.6 | 356 | 2 | Q8KAI9_BUCAP | q8kai9 buchnera ap |
| 363 | 79 | 6.6 | 356 | 2 | Q36RI0_MARHY | q36ri0 marinobacte |
| 364 | 79 | 6.6 | 375 | 2 | Q5X814_LEGPA | q5x814 legionella |
| 365 | 79 | 6.6 | 375 | 2 | Q7MG43_VIBVY | q7mg43 vibrio vuln |
| 366 | 79 | 6.6 | 428 | 2 | Q4ZXH6_PSEU2 | q4zxh6 pseudomonas |
| 367 | 79 | 6.6 | 484 | 2 | O887L9_PSESM | o887l9 pseudomonas |
| 368 | 79 | 6.6 | 770 | 2 | Q2ZGP3_CALSA | q2zgp3 caldicellul |
| 369 | 79 | 6.6 | 770 | 2 | Q2JTY0_9CYAN | q2jty0 cyanobacter |
| 370 | 79 | 6.6 | 770 | 2 | Q6NIE0_CORDI | q6nie0 corynebacte |
| 371 | 79 | 6.6 | 828 | 2 | Q5LA24_BACFN | q5la24 bacteroides |
| 372 | 79 | 6.6 | 1232 | 2 | Q64QD3_BACFR | q64qd3 bacteroides |
| 373 | 79 | 6.6 | 1531 | 2 | Q4RGA8_TETNG | q4rga8 tetraodon n |
| 374 | 79 | 6.6 | 1679 | 2 | Q3JBT9_NITOC | q3jbt9 nitrosococc |
| 375 | 79 | 6.6 | 1780 | 2 | Q96L95_HUMAN | q96l95 homo sapien |
| 376 | 79 | 6.6 | 2751 | 2 | O86TB3_CAEBR | o86tb3 caenorhabdi |
| 377 | 79 | 6.6 | 3010 | 2 | Q61T87_CAEBR | q61t87 caenorhabdi |
| 378 | 79 | 6.6 | 3010 | 2 | Q4Y3S8_PLACH | q4y3s8 plasmodium |
| 379 | 78.5 | 6.6 | 229 | 2 | O9J3H8_9HEPC | o9j3h8 hepatitis c |
| 380 | 78.5 | 6.6 | 232 | 2 | Q9GI20_9HEPC | q9gi20 hepatitis c |
| 381 | 78.5 | 6.6 | 239 | 1 | Q353U9_9GAMM | q353u9 methanosarc |
| 382 | 78.5 | 6.6 | 263 | 2 | Q466U5_METBA | q466u5 methanosarc |
| 383 | 78.5 | 6.6 | 266 | 2 | Y350_MYCPN | y350_mycpn mycoplasma |
| 384 | 78.5 | 6.6 | 269 | 2 | Q51PE7_9RODE | q51pe7 perognathus |
| 385 | 78.5 | 6.6 | 277 | 2 | Q42ZF6_PLABE | q42zf6 plasmodium |
| 386 | 78.5 | 6.6 | 292 | 2 | Q92D15_LISIN | q92d15 listeria in |
| 387 | 78.5 | 6.6 | 305 | 2 | Q3WQW4_HALMA | q3wqw4 haloarcula |
| 388 | 78.5 | 6.6 | 313 | 2 | Q5V6V4_HALMA | q5v6v4 haloarcula |
| 389 | 78.5 | 6.6 | 353 | 1 | Q374A4_RHOPA | q374a4 rhodopseudo |
| 390 | 78.5 | 6.6 | 358 | 2 | Q374Q5_RHOPA | q374q5 rhodopseudo |
| 391 | 78.5 | 6.6 | 358 | 2 | Q345Q5_RHOPA | q345q5 rhodopseudo |
| 392 | 78.5 | 6.6 | 366 | 2 | Q9L0B3_STRCO | q9l0b3 streptomyce |
| 393 | 78.5 | 6.6 | 382 | 2 | Q4HJT2_CAMLA | q4hjt2 campylobact |
| 394 | 78.5 | 6.6 | 382 | 2 | Q57288_HAEIN | q57288 haemophilus |
| 395 | 78.5 | 6.6 | 395 | 2 | Q4QJQ5_LISMO | q4qjq5 listeria mo |
| 396 | 78.5 | 6.6 | 396 | 2 | Q4EUL1_LISMO | q4eul1 listeria mo |
| | | | 366 | 2 | Q8A8F8_BACTN | q8a8f8 bacteroides |
| | | | 382 | 2 | Q5LE17_BACTN | q5le17 bacteroides |
| | | | 382 | 2 | Q64V54_BACFR | q64v54 bacteroides |

| No. | % | pI | Len | N | Accession | Organism | Accession 2 |
|---|---|---|---|---|---|---|---|
| 397 | 78.5 | 6.6 | 418 | 2 | Q65LP8_BACLD | bacillus li | Q65LP8_BACLD |
| 398 | 78.5 | 6.6 | 451 | 2 | Q65UD5_MANSM | mannheimia | Q65UD5_MANSM |
| 399 | 78.5 | 6.6 | 471 | 1 | 5H72A_CRIGR | cricetulus | P18599 |
| 400 | 78.5 | 6.6 | 512 | 2 | Q8GID7_BRUSU | brucella su | Q8GID7_BRUSU |
| 401 | 78.5 | 6.6 | 538 | 2 | Q4HFH8_CAMCO | campylobact | Q4HFH8_CAMCO |
| 402 | 78.5 | 6.6 | 546 | 2 | Q3TII6_RAT | rattus norv | Q3TII6_RAT |
| 403 | 78.5 | 6.6 | 557 | 2 | Q5CXU4_CRYPV | cryptospori | Q5CXU4_CRYPV |
| 404 | 78.5 | 6.6 | 587 | 2 | Q3D365_STRAG | streptococc | Q3D365_STRAG |
| 405 | 78.5 | 6.6 | 509 | 2 | Q3DHN0_STRAG | streptococc | Q3DHN0_STRAG |
| 406 | 78.5 | 6.6 | 666 | 1 | KUP_STRA5 | streptococc | KUP_STRA5 |
| 407 | 78.5 | 6.6 | 666 | 2 | Q8DZI1_STRAG | streptococc | Q8DZI1_STRAG |
| 408 | 78.5 | 6.6 | 666 | 2 | Q3DMX9_STRAG | streptococc | Q3DMX9_STRAG |
| 409 | 78.5 | 6.6 | 678 | 2 | Q61710_MOUSE | mus musculu | Q61710_MOUSE |
| 410 | 78.5 | 6.6 | 681 | 2 | Q769F3_HUMAN | homo sapien | Q769F3_HUMAN |
| 411 | 78.5 | 6.6 | 683 | 2 | Q769F4_HUMAN | homo sapien | Q769F4_HUMAN |
| 412 | 78.5 | 6.6 | 689 | 2 | Q3Q502_9GAMM | shewanella | Q3Q502_9GAMM |
| 413 | 78.5 | 6.6 | 726 | 2 | Q4UC59_THEAN | theileria a | Q4UC59_THEAN |
| 414 | 78.5 | 6.6 | 766 | 2 | ABCB9_HUMAN | homo sapien | Q9NP78 |
| 415 | 78.5 | 6.6 | 766 | 1 | Q6P2Q0_HUMAN | homo sapien | Q6P2Q0_HUMAN |
| 416 | 78.5 | 6.6 | 796 | 2 | Q5W9G7_HUMAN | homo sapien | Q5W9G7_HUMAN |
| 417 | 78.5 | 6.6 | 867 | 2 | Q4N908_THEPA | theileria p | Q4N908_THEPA |
| 418 | 78.5 | 6.6 | 1308 | 2 | Q4XVA2_PLACH | plasmodium | Q4XVA2_PLACH |
| 419 | 78.5 | 6.6 | 6473 | 2 | Q8IKH9_PLAF7 | plasmodium | Q8IKH9_PLAF7 |
| 420 | 78 | 6.6 | 188 | 2 | Q81YM2_BACAN | bacillus an | Q81YM2_BACAN |
| 421 | 78 | 6.6 | 219 | 2 | Q8W2Y0_ORYSA | oryza sativ | Q8W2Y0_ORYSA |
| 422 | 78 | 6.6 | 226 | 2 | Q7T829_9CORO | infectious | Q7T829_9CORO |
| 423 | 78 | 6.6 | 240 | 2 | Q9CPF6_PASMU | pasteurella | Q9CPF6_PASMU |
| 424 | 78 | 6.6 | 245 | 2 | P94625_CLODI | clostridium | P94625_CLODI |
| 425 | 78 | 6.6 | 252 | 2 | Q6B8K2_GRATL | gracilaria | Q6B8K2_GRATL |
| 426 | 78 | 6.6 | 259 | 1 | Q9KD13_BACHD | bacillus ha | Q9KD13_BACHD |
| 427 | 78 | 6.6 | 298 | 2 | Q48BH2_PSE14 | pseudomonas | Q48BH2_PSE14 |
| 428 | 78 | 6.6 | 299 | 2 | Q2KXZ7_BORAV | bordetella | Q2KXZ7_BORAV |
| 429 | 78 | 6.6 | 321 | 2 | Q96XC4_SULTO | sulfolobus | Q96XC4_SULTO |
| 430 | 78 | 6.6 | 339 | 2 | Q8D4K9_VIBVU | vibrio vuln | Q8D4K9_VIBVU |
| 431 | 78 | 6.6 | 345 | 2 | Q2AV5_9GAMM | shewanella | Q2AV5_9GAMM |
| 432 | 78 | 6.6 | 357 | 2 | Q2ZAV5_9GAMM | shewanella | Q2ZAV5_9GAMM |
| 433 | 78 | 6.6 | 360 | 2 | Q97HC3_CLOAB | clostridium | Q97HC3_CLOAB |
| 434 | 78 | 6.6 | 382 | 2 | Q51A3_TETTH | tetrahymena | Q51A3_TETTH |
| 435 | 78 | 6.6 | 414 | 2 | Q8TN61_METAC | methanosarc | Q8TN61_METAC |
| 436 | 78 | 6.6 | 428 | 2 | Q8D5Y9_VIBVU | vibrio vuln | Q8D5Y9_VIBVU |
| 437 | 78 | 6.6 | 431 | 2 | Q9JRS0_ACTAC | actinobacil | Q9JRS0_ACTAC |
| 438 | 78 | 6.6 | 442 | 2 | Q7MD08_VIBVY | vibrio vuln | Q7MD08_VIBVY |
| 439 | 78 | 6.6 | 452 | 2 | Q36DZ4_9GAMM | shewanella | Q36DZ4_9GAMM |
| 440 | 78 | 6.6 | 471 | 1 | Y872_HAEIN | haemophilus | Y872_HAEIN |
| 441 | 78 | 6.6 | 486 | 2 | Q6HMA8_BACHK | bacillus th | Q6HMA8_BACHK |
| 442 | 78 | 6.6 | 494 | 2 | Q3N6A0_9DELT | syntrophoba | Q3N6A0_9DELT |
| 443 | 78 | 6.6 | 545 | 2 | Q6FSM9_CANGA | candida gla | Q6FSM9_CANGA |
| 444 | 78 | 6.6 | 638 | 2 | Q2U024_9CHLR | uncultured | Q2U024_9CHLR |
| 445 | 78 | 6.6 | 641 | 2 | Q9LIC2_ARATH | arabidopsis | Q9LIC2_ARATH |
| 446 | 78 | 6.6 | 650 | 2 | Q2YZ60_STAAB | staphylococ | Q2YZ60_STAAB |
| 447 | 78 | 6.6 | 658 | 2 | Q7QGQ8_ANOGA | anopheles g | Q7QGQ8_ANOGA |
| 448 | 78 | 6.6 | 688 | 2 | Q98M77_RHILO | rhizobium l | Q98M77_RHILO |
| 449 | 78 | 6.6 | 748 | 2 | Q420Y8_DESHA | desulfitoba | Q420Y8_DESHA |
| 450 | 78 | 6.6 | 1042 | 2 | Q3SDA8_PARTE | paramecium | Q3SDA8_PARTE |
| 451 | 78 | 6.6 | 1088 | 2 | Q43RR2_SOLUS | solibacter | Q43RR2_SOLUS |
| 452 | 78 | 6.6 | 1297 | 2 | Q9Y817_SCHPO | schizosacch | Q9Y817_SCHPO |
| 453 | 78 | 6.5 | 2136 | 2 | YCF2_MARPO | marchantia | YCF2_MARPO |
| 454 | 78 | 6.5 | 7180 | 1 | R1AB_CVMJH | m replicase | P19751 |
| 455 | 77.5 | 6.5 | 176 | 2 | Q976T7_SULTO | sulfolobus | Q976T7_SULTO |
| 456 | 77.5 | 6.5 | 190 | 2 | Q9KIA8_ECOLI | escherichia | Q9KIA8_ECOLI |
| 457 | 77.5 | 6.5 | 263 | 2 | Q4MQY0_BACCE | bacillus ce | Q4MQY0_BACCE |
| 458 | 77.5 | 6.5 | 263 | 2 | Q81I83_BACC1 | bacillus ce | Q81I83_BACC1 |
| 459 | 77.5 | 6.5 | 263 | 2 | Q73DX2_BACC1 | bacillus ce | Q73DX2_BACC1 |
| 460 | 77.5 | 6.5 | 266 | 2 | Q5IPF6_PERLO | perognathus | Q5IPF6_PERLO |
| 461 | 77.5 | 6.5 | 269 | 2 | Q3EXW2_BACTI | bacillus th | Q3EXW2_BACTI |
| 462 | 77.5 | 6.5 | 269 | 2 | Q4EV75_LISMO | listeria mo | Q4EV75_LISMO |
| 463 | 77.5 | 6.5 | 270 | 2 | Q8Y8T5_LISMO | listeria mo | Q8Y8T5_LISMO |
| 464 | 77.5 | 6.5 | 270 | 2 | Q8HIY1_PERLO | perognathus | Q8HIY1_PERLO |
| 465 | 77.5 | 6.5 | 270 | 2 | Q8HIY2_PERLO | perognathus | Q8HIY2_PERLO |
| 466 | 77.5 | 6.5 | 270 | 2 | Q8HIY3_PERLO | perognathus | Q8HIY3_PERLO |
| 467 | 77.5 | 6.5 | 294 | 2 | Q8HIY4_PERLO | perognathus | Q8HIY4_PERLO |
| 468 | 77.5 | 6.5 | 294 | 2 | Q8ET30_OCEIH | oceanobacil | Q8ET30_OCEIH |
| 469 | 77.5 | 6.5 | 299 | 2 | Q66FT9_YERPS | yersinia ps | Q66FT9_YERPS |
| 470 | 77.5 | 6.5 | 299 | 2 | Q82ZAL1_YERPE | yersinia pe | Q8ZAL1_YERPE |
| 471 | 77.5 | 6.5 | 310 | 2 | Q8D1I6_YERPE | yersinia pe | Q8D1I6_YERPE |
| 472 | 77.5 | 6.5 | 327 | 2 | Q9PQG1_UREPA | ureaplasma | Q9PQG1_UREPA |
| 473 | 77.5 | 6.5 | 328 | 2 | Q9K686_BACHD | bacillus ha | Q9K686_BACHD |
| 474 | 77.5 | 6.5 | 347 | 2 | Q42882_SCHPO | schizosacch | Q42882_SCHPO |
| 475 | 77.5 | 6.5 | 365 | 2 | Q4AFU3_9CHLB | chlorobium | Q4AFU3_9CHLB |
| 476 | 77.5 | 6.5 | 377 | 2 | Q8R770_THETN | thermoanaer | Q8R770_THETN |
| 477 | 77.5 | 6.5 | 377 | 2 | Q4R1V7_VARHI | varnula hil | Q4R1V7_VARHI |
| 478 | 77.5 | 6.5 | 377 | 2 | Q4R1X9_VARHI | varnula hil | Q4R1X9_VARHI |
| 479 | 77.5 | 6.5 | 377 | 2 | Q4R264_VARHI | varnula hil | Q4R264_VARHI |
| 480 | 77.5 | 6.5 | 377 | 2 | Q4R2A7_VARHI | varnula hil | Q4R2A7_VARHI |
| 481 | 77.5 | 6.5 | 377 | 2 | Q4R2P5_VARHI | varnula hil | Q4R2P5_VARHI |
| 482 | 77.5 | 6.5 | 379 | 2 | Q4R2P6_VARHI | varnula hil | Q4R2P6_VARHI |
| 483 | 77.5 | 6.5 | 384 | 2 | Q48008_PERLO | perognathus | Q48008_PERLO |
| 484 | 77.5 | 6.5 | 392 | 2 | Q2WUY0_CLOBE | clostridium | Q2WUY0_CLOBE |
| 485 | 77.5 | 6.5 | 411 | 2 | Q8G7P7_BIFLO | bifidobacte | Q8G7P7_BIFLO |
| 486 | 77.5 | 6.5 | 416 | 2 | Q9P6N5_SCHPO | schizosacch | Q9P6N5_SCHPO |
| 487 | 77.5 | 6.5 | 422 | 2 | Q4YTQ0_PLABE | plasmodium | Q4YTQ0_PLABE |
| 488 | 77.5 | 6.5 | 430 | 2 | Q9HKX6_THEAC | thermoplasm | Q9HKX6_THEAC |
| 489 | 77.5 | 6.5 | 440 | 2 | Q5WUJ7_LEGPL | legionella | Q5WUJ7_LEGPL |
| 490 | 77.5 | 6.5 | 458 | 2 | Q2ZY23_PEDMN | pedimomonas | Q2ZY23_PEDMN |
| 491 | 77.5 | 6.5 | 481 | 2 | Q62XT1_BACLD | bacillus li | Q62XT1_BACLD |
| 492 | 77.5 | 6.5 | 483 | 2 | Q4P6B0_USTMA | ustilago ma | Q4P6B0_USTMA |
| 493 | 77.5 | 6.5 | 491 | 2 | Q9G8V8_9CRYP | rhodomonas | Q9G8V8_9CRYP |
| 494 | 77.5 | 6.5 | 491 | 2 | Q28284_ARCFU | archaeoglob | Q28284_ARCFU |
| 495 | 77.5 | 6.5 | 495 | 2 | Q6SX10_HCMV | human cytom | Q6SX10_HCMV |
| 496 | 77.5 | 6.5 | 496 | 2 | Q59P22_CANAL | candida alb | Q59P22_CANAL |
| 497 | 77.5 | 6.5 | 497 | 2 | Q4XZG8_PLACH | plasmodium | Q4XZG8_PLACH |
| 498 | 77.5 | 6.5 | 498 | 2 | Q7RNK0_PLAYO | plasmodium | Q7RNK0_PLAYO |
| 499 | 77.5 | 6.5 | 499 | 2 | Q89232_VARV | variola vir | Q89232_VARV |
| 500 | 77.5 | 6.5 | 500 | 2 | Q89180_VARV | variola vir | Q89180_VARV |
| 501 | 77.5 | 6.5 | 543 | 2 | Q2R1U9_ORYSA | oryza sativ | Q2R1U9_ORYSA |
| 502 | 77.5 | 6.5 | 548 | 2 | Q2R1U9_ORYSA | oryza sativ | Q2R1U9_ORYSA |
| 503 | 77.5 | 6.5 | 556 | 2 | Q4HPP2_CAMUP | campylobact | Q4HPP2_CAMUP |
| 504 | 77.5 | 6.5 | 556 | 2 | Q2ZED8_CALSA | caldicellul | Q2ZED8_CALSA |
| 505 | 77.5 | 6.5 | 567 | 2 | Q3VJ85_9CHLB | pelodictyon | Q3VJ85_9CHLB |
| 506 | 77.5 | 6.5 | 572 | 2 | Q2YNB5_BRUAB | brucella ab | Q2YNB5_BRUAB |
| 507 | 77.5 | 6.5 | 618 | 2 | Q8YGI2_BRUME | brucella me | Q8YGI2_BRUME |
| 508 | 77.5 | 6.5 | 620 | 2 | Q73A28_BACCI | bacillus ce | Q73A28_BACCI |
| 509 | 77.5 | 6.5 | 654 | 2 | Q4RUC9_TETNG | tetraodon n | Q4RUC9_TETNG |
| 510 | 77.5 | 6.5 | 676 | 2 | Q3MXT8_9DELT | syntrophoba | Q3MXT8_9DELT |
| 511 | 77.5 | 6.5 | 734 | 1 | NU5C_ORYSA | oryza sativ | P12129 |
| 512 | 77.5 | 6.5 | 788 | 2 | Q3VJ85_9CHLB | pelodictyon | Q3VJ85_9CHLB |
| 513 | 77.5 | 6.5 | 892 | 1 | VP4A_VARV | variola vir | P33817 |
| 514 | 77.5 | 6.5 | 892 | 2 | Q9QNI0_VARV | variola min | Q9QNI0_VARV |
| 515 | 77.5 | 6.5 | 892 | 2 | Q7MLV5_VIBVY | vibrio vuln | Q7MLV5_VIBVY |
| 516 | 77.5 | 6.5 | 979 | 2 | Q5BL65_XENTR | xenopus tro | Q5BL65_XENTR |
| 517 | 77.5 | 6.5 | 1033 | 2 | Q5CTR7_CRYPV | cryptospori | Q5CTR7_CRYPV |
| 518 | 77.5 | 6.5 | 1140 | 2 | Q8ST66_DICDI | dictyosteli | Q8ST66_DICDI |
| 519 | 77.5 | 6.5 | 1476 | 2 | Q25377_LOLOP | loligo opal | Q25377_LOLOP |
| 520 | 77.5 | 6.5 | 1784 | 2 | Q5Z5B8_ORYSA | oryza sativ | Q5Z5B8_ORYSA |
| 521 | 77.5 | 6.5 | 1959 | 2 | Q869H2_LYMST | lymnaea sta | Q869H2_LYMST |
| 522 | 77.5 | 6.5 | 2141 | 1 | Q869H2 | lymnaea sta | Q869H2 |
| 523 | 77.5 | 6.4 | 6680 | 2 | Q5CXT7_CRYPV | cryptospori | Q5CXT7_CRYPV |
| 524 | 77.5 | 6.4 | 160 | 2 | Q72UC4_LEPIC | leptospira | Q72UC4_LEPIC |
| 525 | 77.5 | 6.4 | 170 | 2 | Q8F0Q4_LEPIN | leptospira | Q8F0Q4_LEPIN |
| 526 | 77 | 6.4 | 170 | 2 | Q3VS16_PROAE | prosthecoch | Q3VS16_PROAE |
| 527 | 77 | 6.4 | 191 | 2 | Q3LWE2_CHLS6 | chlo_rarachn | Q3LWE2_CHLS6 |
| 528 | 77 | 6.4 | 200 | 2 | Q33VA0_9GAMM | shewanella | Q33VA0_9GAMM |
| 529 | 77 | 6.4 | 226 | 2 | Q2Z645_9GAMM | shewanella | Q2Z645_9GAMM |
| 530 | 77 | 6.4 | 249 | 2 | Q98VN5_EAV | equine arte | Q98VN5_EAV |
| 531 | 77 | 6.4 | 255 | 2 | Q3EU30_BACTI | bacillus th | Q3EU30_BACTI |
| 532 | 77 | 6.4 | 280 | 2 | Q61082_BACAN | bacillus an | Q61082_BACAN |
| 533 | 77 | 6.4 | 286 | 2 | Q73A28_BACCI | bacillus ce | Q73A28_BACCI |
| 534 | 77 | 6.4 | 286 | 2 | Q54LT2_DICDI | dictyosteli | Q54LT2_DICDI |
| 535 | 77 | 6.4 | 287 | 2 | Q3GB03_9FIRM | syntrophomo | Q3GB03_9FIRM |
| 536 | 77 | 6.4 | 288 | 2 | Q4HFE7_CAMCO | campylobact | Q4HFE7_CAMCO |
| 537 | 77 | 6.4 | 288 | 2 | Q9XTH3_CAEEL | caenorhabdi | Q9XTH3_CAEEL |
| 538 | 77 | 6.4 | 315 | 2 | Q2NSZ8_SODGL | sodalis glo | Q2NSZ8_SODGL |
| 539 | 77 | 6.4 | 332 | 1 | MTR1A_MOUSE | mus musculu | Q61184 |
| 540 | 77 | 6.4 | 346 | 2 | Q4EL37_LISMO | listeria mo | Q4EL37_LISMO |
| 541 | 77 | 6.4 | 353 | 2 | Q8WEK6_THOTA | thomomys ta | Q8WEK6_THOTA |
| 542 | 77 | 6.4 | 383 | 2 | Q8TZC2_METKA | methanopyru | Q8TZC2_METKA |

| No. | Score | E | Length | N | Accession | Organism |
|---|---|---|---|---|---|---|
| 543 | 77 | 6.4 | 386 | 2 | Q7MXQ0_PORGI | porphyromon |
| 544 | 77 | 6.4 | 419 | 2 | P94949_METKA | methanopyru |
| 545 | 77 | 6.4 | 423 | 2 | Q71XS8_LISMF | listeria mo |
| 546 | 77 | 6.4 | 430 | 2 | Q8UIZ6_PYRFU | pyrococcus |
| 547 | 77 | 6.4 | 435 | 2 | Q73RD9_TREDE | treponema d |
| 548 | 77 | 6.4 | 444 | 2 | Q6GD70_STAAS | staphylococ |
| 549 | 77 | 6.4 | 444 | 2 | Q8NYX5_STAAW | staphylococ |
| 550 | 77 | 6.4 | 473 | 2 | Q3GS79_9GAMM | psychrobact |
| 551 | 77 | 6.4 | 477 | 2 | Q2SJ57_9GAMM | hahella che |
| 552 | 77 | 6.4 | 481 | 2 | Q4WQW3_ASPFU | aspergillus |
| 553 | 77 | 6.4 | 490 | 2 | O14670_HUMAN | homo sapien |
| 554 | 77 | 6.4 | 491 | 2 | Q9T251_PHYIN | phytophthor |
| 555 | 77 | 6.4 | 505 | 2 | Q4UIS6_THEAN | theileria a |
| 556 | 77 | 6.4 | 519 | 2 | Q9ASQ7_ARATH | arabidopsis |
| 557 | 77 | 6.4 | 537 | 2 | Q518N5_ENTHI | entamoeba h |
| 558 | 77 | 6.4 | 559 | 2 | Q9AAX4_CAUCR | caulobacter |
| 559 | 77 | 6.4 | 590 | 1 | NU5M_TRYBB | trypanosoma |
| 560 | 77 | 6.4 | 606 | 2 | Q2IFP2_9DELT | anaeromyxob |
| 561 | 77 | 6.4 | 616 | 2 | Q5W2R7_SULIS | sulfolobus |
| 562 | 77 | 6.4 | 650 | 2 | Q5HCQ6_STAAC | staphylococ |
| 563 | 77 | 6.4 | 650 | 2 | Q6G633_STAAS | staphylococ |
| 564 | 77 | 6.4 | 650 | 2 | Q6GDG1_STAAR | staphylococ |
| 565 | 77 | 6.4 | 650 | 2 | Q7A374_STAAN | staphylococ |
| 566 | 77 | 6.4 | 650 | 2 | Q8NUK4_STAAW | staphylococ |
| 567 | 77 | 6.4 | 650 | 2 | Q99QZ7_STAAM | staphylococ |
| 568 | 77 | 6.4 | 722 | 2 | Q632R1_BACCZ | bacillus ce |
| 569 | 77 | 6.4 | 738 | 2 | Q8L838_ARATH | arabidopsis |
| 570 | 77 | 6.4 | 789 | 1 | FTSK_STAAW | staphylococ |
| 571 | 77 | 6.4 | 789 | 1 | FTSK_STAAS | staphylococ |
| 572 | 77 | 6.4 | 836 | 2 | Q7Z1F2_PLAFA | plasmodium |
| 573 | 77 | 6.4 | 877 | 2 | Q750H8_ASHGO | ashbya goss |
| 574 | 77 | 6.4 | 991 | 2 | Q81330_ARATH | arabidopsis |
| 575 | 77 | 6.4 | 1024 | 2 | Q7Z1F1_PLAFA | plasmodium |
| 576 | 77 | 6.4 | 1024 | 2 | Q81KZ6_PLAF7 | plasmodium |
| 577 | 77 | 6.4 | 1025 | 2 | Q25693_PLAFA | plasmodium |
| 578 | 77 | 6.4 | 1117 | 2 | Q9M133_ARATH | arabidopsis |
| 579 | 77 | 6.4 | 1137 | 2 | Q44PG0_CHLLI | chlorobium |
| 580 | 77 | 6.4 | 1477 | 2 | Q6FTR9_CANGA | candida gla |
| 581 | 77 | 6.4 | 1500 | 2 | Q92U84_ARATH | arabidopsis |
| 582 | 77 | 6.4 | 1814 | 2 | O60WH4_CAEBR | caenorhabdi |
| 583 | 77 | 6.4 | 3010 | 2 | O60788_9HEPC | hepatitis c |
| 584 | 77 | 6.4 | 3010 | 2 | O81757_9HEPC | hepatitis c |
| 585 | 77 | 6.4 | 3010 | 2 | Q9J3G4_9HEPC | hepatitis c |
| 586 | 77 | 6.4 | 3013 | 2 | Q6J6P5_9HEPC | hepatitis c |
| 587 | 77 | 6.4 | 4416 | 2 | Q9J3F3_9CORO | murine hepa |
| 588 | 77 | 6.4 | 4416 | 2 | Q9J3F8_9CORO | murine hepa |
| 589 | 77 | 6.4 | 7124 | 1 | R1AB_CVM2 | murine hepa |
| 590 | 76.5 | 6.4 | 189 | 2 | Q9PYA3 | m replicase |
| 591 | 76.5 | 6.4 | 234 | 2 | Q3WSO1_9RHIZ | mesorhizobi |
| 592 | 76.5 | 6.4 | 253 | 2 | Q3W1WO_9ACTO | frankia sp. |
| 593 | 76.5 | 6.4 | 266 | 2 | Q5IPE6_PERLO | perognathus |
| 594 | 76.5 | 6.4 | 278 | 2 | Q8XBF0_ECO57 | escherichia |
| 595 | 76.5 | 6.4 | 281 | 2 | Q8SKS9_9BILA | acylostoma |
| 596 | 76.5 | 6.4 | 282 | 2 | Q92WV5_RHIME | rhizobium m |
| 597 | 76.5 | 6.4 | 342 | 2 | YOE8_YEAST | saccharomyc |
| 598 | 76.5 | 6.4 | 342 | 2 | Q7Z290_CAEEL | caenorhabdi |
| 599 | 76.5 | 6.4 | 352 | 2 | RNFD_SALTI | salmonella |
| 600 | 76.5 | 6.4 | 352 | 1 | RNFD_SALTY | salmonella |
| 601 | 76.5 | 6.4 | 352 | 2 | Q57PI1_SALCH | salmonella |
| 602 | 76.5 | 6.4 | 352 | 2 | Q5PIC8_SALPA | salmonella |
| 603 | 76.5 | 6.4 | 358 | 2 | Q3Y919_CRYGA | cryptococcu |
| 604 | 76.5 | 6.4 | 379 | 1 | CYB_DIPOR | dipodomys o |
| 605 | 76.5 | 6.4 | 379 | 2 | Q9GBY7_OCHPA | ochotona pa |
| 606 | 76.5 | 6.4 | 379 | 2 | Q5083J_9RODE | perognathus |
| 607 | 76.5 | 6.4 | 379 | 2 | Q508L5_PERLO | perognathus |
| 608 | 76.5 | 6.4 | 380 | 2 | Q508L8_9RODE | dipodomys m |
| 609 | 76.5 | 6.4 | 380 | 2 | Q8HNI7_PRANA | praomys nat |
| 610 | 76.5 | 6.4 | 387 | 2 | Q3VX84_PROAE | prosthecoch |
| 611 | 76.5 | 6.4 | 391 | 2 | Q4SIZ9_TETNG | tetraodon n |
| 612 | 76.5 | 6.4 | 395 | 2 | Q8KHK2_PSEAE | pseudomonas |
| 613 | 76.5 | 6.4 | 415 | 2 | Q5UES7_ECOLI | escherichia |
| 614 | 76.5 | 6.4 | 415 | 2 | Q7UB13_SHIFL | shigella fl |
| 615 | 76.5 | 6.4 | 415 | 2 | Q83PL5_SHIFL | shigella fl |

| No. | Score | E | Length | N | ID | Accession | Organism |
|---|---|---|---|---|---|---|---|
| 616 | 76.5 | 6.4 | 438 | 1 | CLN3_MOUSE | Q61124 | mus musculu |
| 617 | 76.5 | 6.4 | 439 | 2 | Q5LBQ8_BACFN | Q5lbq8 | bacteroides |
| 618 | 76.5 | 6.4 | 439 | 2 | Q64SN0_BACFR | Q64sn0 | bacteroides |
| 619 | 76.5 | 6.4 | 451 | 2 | Q660T8_BORGA | Q660t8 | borrelia ga |
| 620 | 76.5 | 6.4 | 453 | 2 | Q6ZGZ4_ORYSA | Q6zgz4 | oryza sativ |
| 621 | 76.5 | 6.4 | 462 | 2 | Q82V00_NITEU | Q82v00 | nitrosomona |
| 622 | 76.5 | 6.4 | 468 | 1 | YDBM_CAEEL | Q19084 | caenorhabdi |
| 623 | 76.5 | 6.4 | 468 | 2 | Q19084 | Q19084 | caenorhabdi |
| 624 | 76.5 | 6.4 | 490 | 1 | Q3S1M1_CAEEL | Q3s1m1 | caenorhabdi |
| 625 | 76.5 | 6.4 | 490 | 2 | Q6SX39_HCMV | Q6sx39 | human cytom |
| 626 | 76.5 | 6.4 | 491 | 2 | Q6SWP6_HCMV | Q6swp6 | human cytom |
| 627 | 76.5 | 6.4 | 491 | 1 | FLVC2_HUMAN | Q9nbo | homo sapien |
| 628 | 76.5 | 6.4 | 528 | 2 | Q53ZT9_HUMAN | Q53zt9 | homo sapien |
| 629 | 76.5 | 6.4 | 526 | 1 | Q7VP70_HAEDU | Q7vp70 | haemophilus |
| 630 | 76.5 | 6.4 | 538 | 2 | Q9PIV5_CAEBR | Q9piv5 | caenorhabdi |
| 631 | 76.5 | 6.4 | 538 | 2 | Q5HWZ4_CAMJR | Q5hwz4 | campylobact |
| 632 | 76.5 | 6.4 | 555 | 2 | Q9PIV5_CAMJE | Q9piv5 | campylobact |
| 633 | 76.5 | 6.4 | 560 | 2 | Q8NBG4_HUMAN | Q8nbg4 | homo sapien |
| 634 | 76.5 | 6.4 | 570 | 2 | Q72GJ6_HUMAN | Q72gj6 | homo sapien |
| 635 | 76.5 | 6.4 | 584 | 2 | Q627P1_CAEBR | Q627p1 | caenorhabdi |
| 636 | 76.5 | 6.4 | 589 | 2 | Q2ZLN1_HELPJ | Q2zln1 | helicobacte |
| 637 | 76.5 | 6.4 | 614 | 2 | Q92LN1_HELPJ | Q92ln1 | helicobacte |
| 638 | 76.5 | 6.4 | 614 | 2 | Q2V4K0_ARATH | Q2v4k0 | arabidopsis |
| 639 | 76.5 | 6.4 | 614 | 2 | Q577U9_BRUAB | Q577u9 | brucella ab |
| 640 | 76.5 | 6.4 | 615 | 2 | Q8FWB2_BRUSU | Q8fwb2 | brucella su |
| 641 | 76.5 | 6.4 | 649 | 2 | Q2YKG7_BRUA2 | Q2ykg7 | brucella ab |
| 642 | 76.5 | 6.4 | 666 | 2 | Q5JF60_PYRKO | Q5jf60 | pyrococcus |
| 643 | 76.5 | 6.4 | 687 | 2 | Q6KZL4_PICTO | Q6kzl4 | picrophilus |
| 644 | 76.5 | 6.4 | 775 | 2 | Q74520_SCHPO | Q74520 | schizosacch |
| 645 | 76.5 | 6.4 | 839 | 2 | Q8XN80_CLOPE | Q8xn80 | clostridium |
| 646 | 76.5 | 6.4 | 902 | 2 | Q4N6A4_THEPA | Q4n6a4 | theileria p |
| 647 | 76.5 | 6.4 | 909 | 2 | Q918C9_CHICK | Q918c9 | gallus gall |
| 648 | 76.5 | 6.4 | 909 | 2 | Q3XN69_9PROT | Q3xn69 | magnetococc |
| 649 | 76.5 | 6.4 | 1034 | 2 | Q54BU4_DICDI | Q54bu4 | dictyosteli |
| 650 | 76.5 | 6.4 | 1141 | 2 | Q8T9W6_DICDI | Q8t9w6 | dictyosteli |
| 651 | 76.5 | 6.4 | 1228 | 2 | Q4DWH6_TRYCR | Q4dwh6 | trypanosoma |
| 652 | 76.5 | 6.4 | 1485 | 2 | Q2RFN9_MOOTH | Q2rfn9 | moorella th |
| 653 | 76.5 | 6.4 | 1641 | 2 | Q3NBS3_9PROT | Q3nbs3 | nitrosomona |
| 654 | 76.5 | 6.4 | 156 | 1 | Q8EUA2_MYCPE | Q8eua2 | mycoplasma |
| 655 | 76.5 | 6.4 | 201 | 2 | Q6BS27_DEBHA | Q6bs27 | debaryomyce |
| 656 | 76.5 | 6.4 | 210 | 2 | Q81504_9HEPC | Q81504 | hepatitis c |
| 657 | 76.5 | 6.4 | 346 | 2 | Q6MT09_MYCMS | Q6mt09 | mycoplasma |
| 658 | 76.5 | 6.4 | 393 | 2 | Q8PXL0_METMA | Q8pxl0 | methanosarc |
| 659 | 76.5 | 6.4 | 402 | 2 | Q6V7I5_EAV | Q6v7i5 | equine arte |
| 660 | 76.5 | 6.4 | 264 | 2 | Q2LYI0_9DELT | Q2lyi0 | syntrophus |
| 661 | 76.5 | 6.4 | 272 | 2 | Q8R7J2_THETN | Q8r7j2 | caenorhabdi |
| 662 | 76.5 | 6.4 | 292 | 2 | Q8ELU4_OCEIH | Q8elu4 | actinobacil |
| 663 | 76.5 | 6.4 | 325 | 2 | Q9ZZH9_MESAU | Q9zzh9 | pseudomonas |
| 664 | 76.5 | 6.4 | 328 | 2 | Q3B337_PELLD | Q3b337 | grylloblatt |
| 665 | 76.5 | 6.4 | 346 | 1 | NU2M_LOCMI | Nu2m | streptococc |
| 666 | 76.5 | 6.4 | 346 | 2 | Q4H7X1_9DEIO | Q4h7x1 | streptococc |
| 667 | 76.5 | 6.4 | 393 | 2 | Q3LRX3_TARGR | Q3lrx3 | mesocricetu |
| 668 | 76.5 | 6.4 | 402 | 2 | Q21933_CAEEL | Q21933 | leptospira |
| 669 | 76.5 | 6.4 | 425 | 2 | Q9JRS2_ACTAC | Q9jrs2 | leptospira |
| 670 | 76.5 | 6.4 | 264 | 2 | Q2Q1I3_9NEOP | Q2q1i3 | streptococc |
| 671 | 76.5 | 6.4 | 292 | 2 | Q85002_STRPN | Q85002 | trypanosoma |
| 672 | 76.5 | 6.4 | 446 | 2 | Q72SX4_LEPIC | Q72sx4 | homo sapien |
| 673 | 76.5 | 6.4 | 461 | 2 | Q85002_STREP | Q85002 | perilla fru |
| 674 | 76.5 | 6.4 | 474 | 2 | Q72SX4_LEPIN | Q72sx4 | epidermophy |
| 675 | 76.5 | 6.4 | 474 | 2 | Q38SJ6_9TRYP | Q38sj6 | trypanosoma |
| 676 | 76.5 | 6.4 | 484 | 2 | Q38F2K0_LEPIN | Q8f2k0 | deinococcus |
| 677 | 76.5 | 6.4 | 487 | 2 | Q2ZEF8_EPIFL | Q2zef8 | dipodomys o |
| 678 | 76.5 | 6.4 | 519 | 2 | Q852P3_PERFR | Q852p3 | homo sapien |
| 679 | 76.5 | 6.4 | 567 | 2 | Q6NXT6_HUMAN | Q6nxt6 | giardia lam |
| 680 | 76 | 6.4 | 616 | 2 | Q7QWH6_GIALA | Q7qwh6 | anabaena va |
| 681 | 76 | 6.4 | 648 | 2 | Q3MEJ3_ANAVT | Q3mej3 | arabidopsis |
| 682 | 76 | 6.4 | 669 | 2 | Q9LZZ7_ARATH | Q9lzz7 | uncultured |
| 683 | 76 | 6.4 | 699 | 2 | Q6IVM6_9GAMM | Q6ivm6 | uncultured |
| 684 | 76 | 6.4 | 851 | 2 | Q6CK04_KLULA | Q6ck04 | kluyveromyc |
| 685 | 76 | 6.4 | 931 | 2 | Q7NBN0_MYCGA | Q7nbn0 | mycoplasma |
| 686 | 76 | 6.4 | 953 | 2 | Q52S70_ORYSA | Q52s70 | oryza sativ |
| 687 | 76 | 6.4 | 1046 | 2 | Q7PVU9_ANOGA | Q7pvu9 | anopheles g |
| 688 | 76 | 6.4 | 1297 | 2 | Q3XSP4_9PROT | Q3xsp4 | magnetococc |
| | 76 | 6.4 | 1301 | 1 | DHX9_CAEEL | O22307 | caenorhabdi |

| No. | % | | Len | N | Accession | Organism |
|---|---|---|---|---|---|---|
| 689 | 76 | 6.4 | 1409 | 2 | Q4DUZ9_TRYCR | trypanosoma |
| 690 | 76 | 6.4 | 1480 | 1 | CFTR_RABIT | oryctolagus |
| 691 | 76 | 6.4 | 1551 | 2 | Q96WN4_VENIN | venturia in |
| 692 | 76 | 6.4 | 1783 | 2 | Q18698_CAEEL | caenorhabdi |
| 693 | 76 | 6.4 | 1877 | 2 | Q8MQA1_CAEEL | caenorhabdi |
| 694 | 76 | 6.4 | 2009 | 2 | Q7R8P2_PLAYO | plasmodium |
| 695 | 76 | 6.4 | 3010 | 2 | P90191_9HEPC | hepatitis c |
| 696 | 76 | 6.4 | 3010 | 2 | P90191_9HEPC | hepatitis c |
| 697 | 76 | 6.4 | 3010 | 2 | P90193_9HEPC | hepatitis c |
| 698 | 76 | 6.4 | 3010 | 2 | P90194_9HEPC | hepatitis c |
| 699 | 75.5 | 6.3 | 156 | 1 | MTR1A_RAT | rattus norv |
| 700 | 75.5 | 6.3 | 162 | 2 | Q66PG7_XENLA | xenopus lae |
| 701 | 75.5 | 6.3 | 203 | 2 | Q2XP33_BACSU | bacillus su |
| 702 | 75.5 | 6.3 | 206 | 2 | Q61TR8_CAEBR | caenorhabdi |
| 703 | 75.5 | 6.3 | 220 | 2 | Q633A3_BACCZ | bacillus ce |
| 704 | 75.5 | 6.3 | 228 | 2 | Q9VUN8_DROME | drosophila |
| 705 | 75.5 | 6.3 | 231 | 2 | Q6MD11_PARUW | parachlamyd |
| 706 | 75.5 | 6.3 | 244 | 2 | Q6B927_GRATL | gracilaria |
| 707 | 75.5 | 6.3 | 247 | 2 | Q7TPI3_RAT | rattus norv |
| 708 | 75.5 | 6.3 | 248 | 2 | Q63EZ9_BACCZ | bacillus ce |
| 709 | 75.5 | 6.3 | 263 | 2 | Q6HMF5_BACHK | bacillus th |
| 710 | 75.5 | 6.3 | 263 | 2 | Q63GB2_BACCZ | bacillus ce |
| 711 | 75.5 | 6.3 | 263 | 2 | Q6HNS6_BACHK | bacillus th |
| 712 | 75.5 | 6.3 | 263 | 2 | Q81YU8_BACAN | bacillus an |
| 713 | 75.5 | 6.3 | 263 | 2 | Q8CYF4_STRR6 | streptococc |
| 714 | 75.5 | 6.3 | 266 | 2 | Q97PD2_STRPN | streptococc |
| 715 | 75.5 | 6.3 | 269 | 2 | Q5IPF7_9RODE | perognathus |
| 716 | 75.5 | 6.3 | 278 | 2 | Q66PG6_XENLA | xenopus lae |
| 717 | 75.5 | 6.3 | 279 | 2 | Q865K7_MACEU | macropus eu |
| 718 | 75.5 | 6.3 | 282 | 2 | Q3BSJ4_XANCS | xanthomonas |
| 719 | 75.5 | 6.3 | 303 | 2 | Q3A9G4_CARHZ | carboxydoth |
| 720 | 75.5 | 6.3 | 305 | 2 | Q9KZ08_STRCO | streptomyce |
| 721 | 75.5 | 6.3 | 309 | 2 | Q4S7P1_TETNG | tetraodon n |
| 722 | 75.5 | 6.3 | 326 | 2 | Q5C2S1_SCHJA | schistosoma |
| 723 | 75.5 | 6.3 | 339 | 2 | Q9ESJ3_RAT | rattus norv |
| 724 | 75.5 | 6.3 | 342 | 2 | Q9KSB3_VIBCH | vibrio chol |
| 725 | 75.5 | 6.3 | 342 | 2 | Q59TA5_CANAL | candida alb |
| 726 | 75.5 | 6.3 | 352 | 1 | Q9QEV3_HHV8 | human herpe |
| 727 | 75.5 | 6.3 | 352 | 2 | RNFD_ECOLI | escherichia |
| 728 | 75.5 | 6.3 | 352 | 2 | RNFD_ECOS7 | escherichia |
| 729 | 75.5 | 6.3 | 352 | 2 | Q320Y7_SHIBS | shigella bo |
| 730 | 75.5 | 6.3 | 352 | 2 | Q32FE3_SHIDS | shigella dy |
| 731 | 75.5 | 6.3 | 352 | 2 | Q3Z1Y5_SHISS | shigella so |
| 732 | 75.5 | 6.3 | 352 | 2 | Q2MB69_ECOLI | escherichia |
| 733 | 75.5 | 6.3 | 352 | 2 | Q8FH94_ECOL6 | escherichia |
| 734 | 75.5 | 6.3 | 364 | 2 | Q83KY5_SHIFL | shigella fl |
| 735 | 75.5 | 6.3 | 369 | 2 | Q2ULL9_ASPOR | aspergillus |
| 736 | 75.5 | 6.3 | 371 | 2 | Q2ULL9_ASPOR | aspergillus |
| 737 | 75.5 | 6.3 | 377 | 2 | Q3C185_THEET | thermoanaer |
| 738 | 75.5 | 6.3 | 379 | 1 | Q2USP9_ASPOR | aspergillus |
| 739 | 75.5 | 6.3 | 379 | 2 | Q4R2L1_VARHI | vargula hil |
| 740 | 75.5 | 6.3 | 389 | 2 | CYB_ZAPTR | zapus trino |
| 741 | 75.5 | 6.3 | 397 | 2 | Q9XNN1_ZAPTR | zapus trino |
| 742 | 75.5 | 6.3 | 397 | 2 | Q50BJ8_PERFA | perognathus |
| 743 | 75.5 | 6.3 | 400 | 2 | Q8AYS5_HYLJA | hyla japoni |
| 744 | 75.5 | 6.3 | 401 | 2 | Q9N4R5_CAEEL | caenorhabdi |
| 745 | 75.5 | 6.3 | 410 | 2 | Q6RXC2_HCMV | human cytom |
| 746 | 75.5 | 6.3 | 413 | 2 | Q4ZIY5_PLABE | plasmodium |
| 747 | 75.5 | 6.3 | 415 | 1 | Q3SSF2_NITWN | nitrobacter |
| 748 | 75.5 | 6.3 | 415 | 2 | Q70NW4_9BILA | strongyloid |
| 749 | 75.5 | 6.3 | 415 | 2 | Q5UET7_ECOLI | escherichia |
| 750 | 75.5 | 6.3 | 415 | 2 | Q5UEU4_ECOLI | escherichia |
| 751 | 75.5 | 6.3 | 415 | 1 | TNAB_ECO57 | escherichia |
| 752 | 75.5 | 6.3 | 417 | 2 | TNAB_ECOLI | escherichia |
| 753 | 75.5 | 6.3 | 421 | 2 | P23173_ECOLI | escherichia |
| 754 | 75.5 | 6.3 | 430 | 2 | Q31UW3_SHIBS | shigella bo |
| 755 | 75.5 | 6.3 | 433 | 2 | Q8FBV1_ECOL6 | escherichia |
| 756 | 75.5 | 6.3 | 446 | 2 | Q2VTE8_APLCA | aplysia cal |
| 757 | 75.5 | 6.3 | 466 | 2 | Q2P2G3_XANOR | xanthomonas |
| 758 | 75.5 | 6.3 | 471 | 2 | Q5X337_LEGPA | legionella |
| 759 | 75.5 | 6.3 | 471 | 2 | Q6F3C9_CAEEL | caenorhabdi |
| 760 | 75.5 | 6.3 | 481 | 2 | Q6F8U0_CAEEL | caenorhabdi |
| 761 | 75.5 | 6.3 | 482 | 2 | Q9P6J0_SCHPO | schizosacch |

| No. | % | | Len | N | Accession | Organism |
|---|---|---|---|---|---|---|
| 762 | 75.5 | 6.3 | 491 | 2 | Q6SWJ1_HCMV | human cytom |
| 763 | 75.5 | 6.3 | 491 | 2 | Q6SWS4_HCMV | human cytom |
| 764 | 75.5 | 6.3 | 491 | 2 | Q6SWW2_HCMV | human cytom |
| 765 | 75.5 | 6.3 | 491 | 2 | Q6SWY1_HCMV | human cytom |
| 766 | 75.5 | 6.3 | 498 | 2 | Q47543_CHLEU | chlamydomon |
| 767 | 75.5 | 6.3 | 501 | 2 | Q6CH25_YARLI | yarrowia li |
| 768 | 75.5 | 6.3 | 521 | 2 | Q40JQ8_EHRCH | ehrlichia c |
| 769 | 75.5 | 6.3 | 539 | 2 | Q5CI52_CRYPV | cryptospori |
| 770 | 75.5 | 6.3 | 551 | 1 | Q91X85_MOUSE | mus muscu |
| 771 | 75.5 | 6.3 | 551 | 2 | Q2Z9L7_9GAMM | shewanella |
| 772 | 75.5 | 6.3 | 574 | 2 | Q36GT8_9GAMM | shewanella |
| 773 | 75.5 | 6.3 | 593 | 2 | Q25322_HELPY | helicobacte |
| 774 | 75.5 | 6.3 | 646 | 2 | Q52LM5_CHICK | gallus gall |
| 775 | 75.5 | 6.3 | 708 | 2 | Q22806_CAEEL | caenorhabdi |
| 776 | 75.5 | 6.3 | 746 | 2 | Q8PGM4_XANAC | xanthomonas |
| 777 | 75.5 | 6.3 | 773 | 2 | Q96325_ARATH | arabidopsis |
| 778 | 75.5 | 6.3 | 773 | 1 | CLCA_ARATH | arabidopsis |
| 779 | 75.5 | 6.3 | 795 | 2 | P92941_ARATH | arabidopsis |
| 780 | 75.5 | 6.3 | 939 | 2 | Q61FI6_CAEBR | caenorhabdi |
| 781 | 75.5 | 6.3 | 1008 | 2 | Q5BG34_EMENI | emericella |
| 782 | 75.5 | 6.3 | 1010 | 2 | Q89154_9HEPC | hepatitis c |
| 783 | 75.5 | 6.3 | 1088 | 2 | Q3HAL4_TRIER | trichodesmi |
| 784 | 75.5 | 6.3 | 1142 | 2 | Q4UI92_THEAN | theileria a |
| 785 | 75.5 | 6.3 | 1583 | 2 | Q9UT41_SCHPO | schizosacch |
| 786 | 75.5 | 6.3 | 3010 | 2 | Q7P9S4_RICSI | rickettsia |
| 787 | 75 | 6.3 | 105 | 2 | Q9J3G7_9HEPC | hepatitis c |
| 788 | 75 | 6.3 | 132 | 2 | Q5AM04_CANAL | candida alb |
| 789 | 75 | 6.3 | 152 | 2 | Q6N505_RHOPA | rhodopseudo |
| 790 | 75 | 6.3 | 152 | 2 | Q2N8U7_9SPHN | erythrobact |
| 791 | 75 | 6.3 | 156 | 2 | O81498_9HEPC | hepatitis c |
| 792 | 75 | 6.3 | 156 | 2 | O81507_9HEPC | hepatitis c |
| 793 | 75 | 6.3 | 156 | 2 | O81531_9HEPC | hepatitis c |
| 794 | 75 | 6.3 | 170 | 2 | O81531_9HEPC | hepatitis c |
| 795 | 75 | 6.3 | 194 | 2 | Q3J4F0_RHOS4 | rhodobacter |
| 796 | 75 | 6.3 | 202 | 2 | Q36M19_MARHY | marinobacte |
| 797 | 75 | 6.3 | 215 | 2 | Q34238_CAPSU | capricornis |
| 798 | 75 | 6.3 | 215 | 2 | Q336X2_ORYSA | oryza sativ |
| 799 | 75 | 6.3 | 218 | 2 | Q41999_STAHU | staphylococ |
| 800 | 75 | 6.3 | 220 | 2 | Q6SKB1_ARTAU | arthrobacte |
| 801 | 75 | 6.3 | 225 | 2 | Q5FF13_EHRRG | ehrlichia r |
| 802 | 75 | 6.3 | 225 | 2 | Q6VMD0_9CORO | coronavirus |
| 803 | 75 | 6.3 | 227 | 2 | Q9GAT3_OCHON | ochotona hy |
| 804 | 75 | 6.3 | 227 | 2 | Q3RXW8_RALME | ralstonia m |
| 805 | 75 | 6.3 | 228 | 2 | Q4YQG6_PLABE | plasmodium |
| 806 | 75 | 6.3 | 232 | 2 | Q3CFK0_THEET | thermoanaer |
| 807 | 75 | 6.3 | 249 | 1 | Y1368_METJA | methanococc |
| 808 | 75 | 6.3 | 256 | 2 | Q631U3_BACCZ | bacillus ce |
| 809 | 75 | 6.3 | 273 | 2 | Q3VLP9_9CHLB | pelodictyon |
| 810 | 75 | 6.3 | 274 | 2 | Q9KND0_VIBCH | vibrio chol |
| 811 | 75 | 6.3 | 277 | 2 | Q6MN43_BDEBA | bdellovibri |
| 812 | 75 | 6.3 | 280 | 2 | Q44K03_CHRSL | chromohalob |
| 813 | 75 | 6.3 | 294 | 2 | Q8RET4_FUSNN | fusobacteri |
| 814 | 75 | 6.3 | 302 | 2 | Q6CVK2_KLULA | kluyveromyc |
| 815 | 75 | 6.3 | 311 | 2 | Q52LG8_CHICK | gallus gall |
| 816 | 75 | 6.3 | 318 | 2 | Q4SMC3_TETNG | tetraodon n |
| 817 | 75 | 6.3 | 330 | 2 | Q58239_PYRHO | pyrococcus |
| 818 | 75 | 6.3 | 368 | 2 | Q467V3_METBA | methanosarc |
| 819 | 75 | 6.3 | 371 | 2 | Q3TS71_MOUSE | mus muscu |
| 820 | 75 | 6.3 | 371 | 2 | Q8BW45_MOUSE | mus muscu |
| 821 | 75 | 6.3 | 373 | 1 | PE2R3_PIG | sus scrofa |
| 822 | 75 | 6.3 | 375 | 2 | Q48ME7_PSE14 | pseudomonas |
| 823 | 75 | 6.3 | 380 | 1 | CYB_RANRU | rana rugosa |
| 824 | 75 | 6.3 | 380 | 2 | Q69GJ2_9PERO | nandus nebu |
| 825 | 75 | 6.3 | 387 | 2 | Q46657_PIG | sus scrofa |
| 826 | 75 | 6.3 | 407 | 2 | Q7NRF5_CHRVO | chromobacte |
| 827 | 75 | 6.3 | 418 | 2 | Q6QFB8_LEGPN | legionella |
| 828 | 75 | 6.3 | 418 | 2 | Q6A8T1_PROAC | propionibac |
| 829 | 75 | 6.3 | 418 | 2 | Q6GFB8_LEGPL | legionella |
| 830 | 75 | 6.3 | 418 | 2 | Q5WZ83_LEGPL | legionella |
| 831 | 75 | 6.3 | 424 | 2 | Q5X7T2_LEGPA | legionella |
| 832 | 75 | 6.3 | 425 | 2 | Q2N984_9SPHN | erythrobact |
| 833 | 75 | 6.3 | 460 | 2 | Q4Z7S9_PLABE | plasmodium |
| 834 | 75 | 6.3 | 460 | 2 | Q3JN15_BURP1 | burkholderi |

| No. | % | | Len | N | Accession | Organism |
|---|---|---|---|---|---|---|
| 835 | 75 | 6.3 | 460 | 2 | Q63QA3_BURPS | burkholderi |
| 836 | 75 | 6.3 | 473 | 1 | GBRR1_HUMAN | homo sapien |
| 837 | 75 | 6.3 | 473 | 2 | Q9BX06_HUMAN | homo sapien |
| 838 | 75 | 6.3 | 476 | 2 | Q46N18_RALEJ | ralstonia e |
| 839 | 75 | 6.3 | 488 | 2 | Q7RW58_NEUCR | neurospora |
| 840 | 75 | 6.3 | 498 | 2 | Q75U67_FUGRU | fugu rubrip |
| 841 | 75 | 6.3 | 526 | 2 | Q9SN21_ARATH | arabidopsis |
| 842 | 75 | 6.3 | 543 | 2 | Q7NS50_CHRVO | chromobacte |
| 843 | 75 | 6.3 | 625 | 1 | KUP2_LEGPH | legionella |
| 844 | 75 | 6.3 | 649 | 2 | O34952_BACSU | bacillus su |
| 845 | 75 | 6.3 | 662 | 2 | Q7VED4_PROMA | prochloroco |
| 846 | 75 | 6.3 | 753 | 2 | Q98S90_GUITH | guillardia |
| 847 | 75 | 6.3 | 761 | 2 | Q3GE97_9FIRM | syntrophomo |
| 848 | 75 | 6.3 | 777 | 2 | Q6BG55_PARTE | paramecium |
| 849 | 75 | 6.3 | 834 | 2 | Q2I6B0_RAT | rattus norv |
| 850 | 75 | 6.3 | 838 | 2 | Q4HZA9_GIBZE | gibberella |
| 851 | 75 | 6.3 | 883 | 2 | Q4N4I2_THEPA | theileria p |
| 852 | 75 | 6.3 | 885 | 2 | Q8PU16_METMA | methanosarc |
| 853 | 75 | 6.3 | 937 | 2 | Q82ZR7_ENTFA | enterococcu |
| 854 | 75 | 6.3 | 1008 | 2 | 089152_9HEPC | hepatitis c |
| 855 | 75 | 6.3 | 1008 | 2 | 089153_9HEPC | hepatitis c |
| 856 | 75 | 6.3 | 1008 | 2 | 089156_9HEPC | hepatitis c |
| 857 | 75 | 6.3 | 1131 | 2 | Q8NAT5_HUMAN | homo sapien |
| 858 | 75 | 6.3 | 1145 | 2 | Q8GUE7_9LILI | cymodocea n |
| 859 | 75 | 6.3 | 1146 | 2 | Q31LG0_PSEHT | pseudoalter |
| 860 | 75 | 6.3 | 1154 | 2 | Q6FTI6_CANGA | candida gla |
| 861 | 75 | 6.3 | 1336 | 2 | Q6F1J1_MESFL | mesoplasma |
| 862 | 75 | 6.3 | 1703 | 2 | Q38B01_9TRYP | trypanosoma |
| 863 | 75 | 6.3 | 1704 | 1 | Q95206_9TRYP | trypanosoma |
| 864 | 74.5 | 6.3 | 159 | 2 | Q34A83_RHOPA | rhodopseudo |
| 865 | 75 | 6.3 | 2248 | 1 | CYA1_DROME | drosophila |
| 866 | 75 | 6.3 | 2846 | 2 | Q55EL4_DICDI | dictyosteli |
| 867 | 75 | 6.3 | 3010 | 2 | Q68833_9HEPC | hepatitis c |
| 868 | 75 | 6.3 | 3010 | 2 | Q9J3G2_9HEPC | hepatitis c |
| 869 | 75 | 6.3 | 3010 | 2 | Q9J3G5_9HEPC | hepatitis c |
| 870 | 75 | 6.3 | 3010 | 2 | Q9QIY7_9HEPC | hepatitis c |
| 871 | 75 | 6.3 | 3010 | 2 | Q9QIY8_9HEPC | hepatitis c |
| 872 | 74.5 | 6.2 | 174 | 2 | P32870_DROME | drosophila |
| 873 | 74.5 | 6.2 | 179 | 2 | P97068_9ENTR | salmonella |
| 874 | 74.5 | 6.2 | 180 | 2 | Q8EPH9_OCEIH | oceanobacil |
| 875 | 74.5 | 6.2 | 222 | 2 | P71253_ECOLI | escherichia |
| 876 | 74.5 | 6.2 | 222 | 2 | Q32DT0_SHIDS | shigella dy |
| 877 | 74.5 | 6.2 | 227 | 2 | Q9GAT4_OCHCU | ochotona cu |
| 878 | 74.5 | 6.2 | 227 | 2 | Q9GAT5_OCHTI | ochotona th |
| 879 | 74.5 | 6.2 | 227 | 2 | Q9GAT6_OCHPR | ochotona pr |
| 880 | 74.5 | 6.2 | 258 | 2 | Q88WC7_LACPL | lactobacill |
| 881 | 74.5 | 6.2 | 276 | 2 | Q9R905_RHIME | rhizobium m |
| 882 | 74.5 | 6.2 | 278 | 2 | Q2R1I5_ORYSA | oryza sativ |
| 883 | 74.5 | 6.2 | 280 | 2 | Q6WIF6_SYNP8 | synechococc |
| 884 | 74.5 | 6.2 | 290 | 2 | Q6SEU1_9BACT | uncultured |
| 885 | 74.5 | 6.2 | 294 | 2 | Q4CJI1_CLOTM | clostridium |
| 886 | 74.5 | 6.2 | 298 | 2 | Q6BWD3_DEBHA | debaryomyce |
| 887 | 74.5 | 6.2 | 298 | 2 | Q51EN3_ENTHI | entamoeba h |
| 888 | 74.5 | 6.2 | 313 | 2 | Q8R7K6_THETN | thermoanaer |
| 889 | 74.5 | 6.2 | 335 | 2 | Q9WXS7_THEMA | thermotoga |
| 890 | 74.5 | 6.2 | 346 | 2 | Q5FMX7_LACAC | lactobacill |
| 891 | 74.5 | 6.2 | 355 | 1 | P49238_CX3C1_HUMAN | homo sapien |
| 892 | 74.5 | 6.2 | 358 | 2 | Q5WHM9_BACSK | bacillus cl |
| 893 | 74.5 | 6.2 | 363 | 2 | CX3C1_HUMAN | homo sapien |
| 894 | 74.5 | 6.2 | 364 | 2 | Q48VQ7_STRPM | streptococc |
| 895 | 74.5 | 6.2 | 377 | 2 | Q8IDY2_PLAF7 | plasmodium |
| 896 | 74.5 | 6.2 | 377 | 2 | Q4R1V2_VARHI | vargula hil |
| 897 | 74.5 | 6.2 | 377 | 2 | Q4R1V3_VARHI | vargula hil |
| 898 | 74.5 | 6.2 | 377 | 2 | Q4R1V6_VARHI | vargula hil |
| 899 | 74.5 | 6.2 | 377 | 2 | Q4R1W3_VARHI | vargula hil |
| 900 | 74.5 | 6.2 | 377 | 2 | Q4R1X3_VARHI | vargula hil |
| 901 | 74.5 | 6.2 | 377 | 2 | Q4R1Y1_VARHI | vargula hil |
| 902 | 74.5 | 6.2 | 377 | 2 | Q4R1Y8_VARHI | vargula hil |
| 903 | 74.5 | 6.2 | 377 | 2 | Q4R126_VARHI | vargula hil |
| 904 | 74.5 | 6.2 | 377 | 2 | Q4R128_VARHI | vargula hil |
| 905 | 74.5 | 6.2 | 377 | 2 | Q4R201_VARHI | vargula hil |
| 906 | 74.5 | 6.2 | 377 | 2 | Q4R222_VARHI | vargula hil |
| 907 | 74.5 | 6.2 | 377 | 2 | Q4R223_VARHI | vargula hil |
| 908 | 74.5 | 6.2 | 377 | 2 | Q4R254_VARHI | vargula hil |
| 909 | 74.5 | 6.2 | 377 | 2 | Q4R268_VARHI | vargula hil |
| 910 | 74.5 | 6.2 | 377 | 2 | Q4R273_VARHI | vargula hil |
| 911 | 74.5 | 6.2 | 377 | 2 | Q4R285_VARHI | vargula hil |
| 912 | 74.5 | 6.2 | 377 | 2 | Q4R286_VARHI | vargula hil |
| 913 | 74.5 | 6.2 | 377 | 2 | Q4R288_VARHI | vargula hil |
| 914 | 74.5 | 6.2 | 377 | 2 | Q4R289_VARHI | vargula hil |
| 915 | 74.5 | 6.2 | 377 | 2 | Q4R290_VARHI | vargula hil |
| 916 | 74.5 | 6.2 | 377 | 2 | Q4R292_VARHI | vargula hil |
| 917 | 74.5 | 6.2 | 377 | 2 | Q4R294_VARHI | vargula hil |
| 918 | 74.5 | 6.2 | 377 | 2 | Q4R295_VARHI | vargula hil |
| 919 | 74.5 | 6.2 | 377 | 2 | Q4R296_VARHI | vargula hil |
| 920 | 74.5 | 6.2 | 377 | 2 | Q4R299_VARHI | vargula hil |
| 921 | 74.5 | 6.2 | 377 | 2 | Q4R2A2_VARHI | vargula hil |
| 922 | 74.5 | 6.2 | 377 | 2 | Q4R2A9_VARHI | vargula hil |
| 923 | 74.5 | 6.2 | 377 | 2 | Q4R2B4_VARHI | vargula hil |
| 924 | 74.5 | 6.2 | 377 | 2 | Q4R2C4_VARHI | vargula hil |
| 925 | 74.5 | 6.2 | 377 | 2 | Q4R2C9_VARHI | vargula hil |
| 926 | 74.5 | 6.2 | 377 | 2 | Q4R2D6_VARHI | vargula hil |
| 927 | 74.5 | 6.2 | 377 | 2 | Q4R2E3_VARHI | vargula hil |
| 928 | 74.5 | 6.2 | 377 | 2 | Q4R2E4_VARHI | vargula hil |
| 929 | 74.5 | 6.2 | 377 | 2 | Q4R2E7_VARHI | vargula hil |
| 930 | 74.5 | 6.2 | 377 | 2 | Q4R2F7_VARHI | vargula hil |
| 931 | 74.5 | 6.2 | 377 | 2 | Q4R2G0_VARHI | vargula hil |
| 932 | 74.5 | 6.2 | 377 | 2 | Q4R2G6_VARHI | vargula hil |
| 933 | 74.5 | 6.2 | 377 | 2 | Q4R2H6_VARHI | vargula hil |
| 934 | 74.5 | 6.2 | 377 | 2 | Q4R2H9_VARHI | vargula hil |
| 935 | 74.5 | 6.2 | 377 | 2 | Q4R2I1_VARHI | vargula hil |
| 936 | 74.5 | 6.2 | 377 | 2 | Q4R2J3_VARHI | vargula hil |
| 937 | 74.5 | 6.2 | 377 | 2 | Q4R2J9_VARHI | vargula hil |
| 938 | 74.5 | 6.2 | 377 | 2 | Q4R2K1_VARHI | vargula hil |
| 939 | 74.5 | 6.2 | 377 | 2 | Q4R2K2_VARHI | vargula hil |
| 940 | 74.5 | 6.2 | 377 | 2 | Q4R2K3_VARHI | vargula hil |
| 941 | 74.5 | 6.2 | 377 | 2 | Q4R2K5_VARHI | vargula hil |
| 942 | 74.5 | 6.2 | 377 | 2 | Q4R2K8_VARHI | vargula hil |
| 943 | 74.5 | 6.2 | 377 | 2 | Q4R2M1_VARHI | vargula hil |
| 944 | 74.5 | 6.2 | 377 | 2 | Q4R2M8_VARHI | vargula hil |
| 945 | 74.5 | 6.2 | 377 | 2 | Q4R2N2_VARHI | vargula hil |
| 946 | 74.5 | 6.2 | 377 | 2 | Q4R2N4_VARHI | vargula hil |
| 947 | 74.5 | 6.2 | 377 | 2 | Q4R2N5_VARHI | vargula hil |
| 948 | 74.5 | 6.2 | 377 | 2 | Q4R2N6_VARHI | vargula hil |
| 949 | 74.5 | 6.2 | 377 | 2 | Q4R2P2_VARHI | vargula hil |
| 950 | 74.5 | 6.2 | 377 | 2 | Q4R2P4_VARHI | vargula hil |
| 951 | 74.5 | 6.2 | 379 | 2 | Q9LCN4_MICOL | micromonosp |
| 952 | 74.5 | 6.2 | 379 | 2 | Q4A6X7_MYCSS | mycoplasma |
| 953 | 74.5 | 6.2 | 379 | 2 | Q94AI3_ARATH | arabidopsis |
| 954 | 74.5 | 6.2 | 378 | 1 | ALG10_CANAL | candida alb |
| 955 | 74.5 | 6.2 | 377 | 2 | Q59YY2_ARATH | arabidopsis |
| 956 | 74.5 | 6.2 | 377 | 2 | Q9GB24_OCHPR | ochotona pr |
| 957 | 74.5 | 6.2 | 377 | 2 | Q6DUV8_BRANA | brassica na |
| 958 | 74.5 | 6.2 | 379 | 2 | Q6ELW8_OCHPR | ochotona pr |
| 959 | 74.5 | 6.2 | 379 | 2 | Q8WB05_APLRU | aplodontia |
| 960 | 74.5 | 6.2 | 392 | 2 | Q9B9E3_CHAPN | chaetodipus |
| 961 | 74.5 | 6.2 | 415 | 2 | Q65MD8_BACLD | bacillus li |
| 962 | 74.5 | 6.2 | 442 | 1 | P14842_RAT | rattus norv |
| 963 | 74.5 | 6.2 | 450 | 2 | Q4U3W9_MRSAU | mesocricetu |
| 964 | 74.5 | 6.2 | 458 | 2 | Q9K5Y9_BACHD | bacillus ha |
| 965 | 74.5 | 6.2 | 471 | 2 | Q6QU71_ASPFU | aspergillus |
| 966 | 74.5 | 6.2 | 471 | 2 | Q2G348_SORBI | sorghum bic |
| 967 | 74.5 | 6.2 | 473 | 2 | Q2RU28_RHORU | rhodospiril |
| 968 | 74.5 | 6.2 | 488 | 2 | Q55UE4_CRYNE | cryptococcu |
| 969 | 74.5 | 6.2 | 500 | 2 | Q5K102_CRYNE | cryptococcu |
| 970 | 74.5 | 6.2 | 510 | 2 | Q66GG5_ARATH | arabidopsis |
| 971 | 74.5 | 6.2 | 523 | 2 | Q8N2B3_HUMAN | homo sapien |
| 972 | 74.5 | 6.2 | 523 | 2 | Q2Z454_WHEAT | triticum ae |
| 973 | 74.5 | 6.2 | 540 | 2 | Q4WLQ1_ASPFU | aspergillus |
| 974 | 74.5 | 6.2 | 562 | 2 | Q9VD40_DROME | drosophila |
| 975 | 74.5 | 6.2 | 594 | 1 | P36029_YEAST | saccharomyc |
| 976 | 74.5 | 6.2 | 594 | 2 | Q3IEZ1_PSEHT | pseudoalter |
| 977 | 74.5 | 6.2 | 597 | 2 | Q2ZVR1_SHEPU | shewanella |
| 978 | 74.5 | 6.2 | 615 | 2 | Q361N8_9GAMM | shewanella |
| 979 | 74.5 | 6.2 | 793 | 2 | Q4PCY9_USTMA | ustilago ma |
| 980 | 74.5 | 6.2 | 848 | 2 | Q8VVK9_CORGL | corynebacte |

| No. | | | Len | | ID | Acc | Organism |
|---|---|---|---|---|---|---|---|
| 981 | 74.5 | 6.2 | 990 | 1 | FTSK_VIBVU | Q8dma2 | vibrio vuln |
| 982 | 74.5 | 6.2 | 1004 | 2 | Q3H520_9ACTO | Q3h520 | nocardioide |
| 983 | 74.5 | 6.2 | 1022 | 2 | Q4U8N7_THEAN | Q4u8n7 | theileria a |
| 984 | 74.5 | 6.2 | 1023 | 2 | Q38FL3_9TRYP | Q38fl3 | trypanosoma |
| 985 | 74.5 | 6.2 | 1033 | 2 | Q382A3_9TRYP | Q382a3 | trypanosoma |
| 986 | 74.5 | 6.2 | 1033 | 2 | Q72ZC1_TRYBB | Q72zc1 | trypanosoma |
| 987 | 74.5 | 6.2 | 1034 | 2 | Q72ZC0_9TRYP | Q72zc0 | trypanosoma |
| 988 | 74.5 | 6.2 | 1183 | 2 | Q9447_CALVI | Q9447 | calliphora |
| 989 | 74.5 | 6.2 | 1401 | 2 | Q61PW5_CAEBR | Q61pw5 | caenorhabdi |
| 990 | 74.5 | 6.2 | 1520 | 2 | Q8T687_DICDI | Q8t687 | dictyosteli |
| 991 | 74.5 | 6.2 | 1534 | 2 | Q54TV1_DICDI | Q54tv1 | dictyosteli |
| 992 | 74.5 | 6.2 | 1559 | 2 | Q7S0S1_NEUCR | Q7s0s1 | neurospora |
| 993 | 74.5 | 6.2 | 1640 | 2 | Q54Z25_DICDI | Q54z25 | dictyosteli |
| 994 | 74.5 | 6.2 | 1808 | 2 | Q9LYS6_ARATH | Q9lys6 | arabidopsis |
| 995 | 74.5 | 6.2 | 1837 | 2 | Q8IKF1_PLAF7 | Q8ikf1 | plasmodium |
| 996 | 74.5 | 6.2 | 3010 | 2 | Q8IKF1_PLAF7 | Q8ikf1 | plasmodium |
| 997 | 74.5 | 6.2 | 124 | 2 | Q91AU0_9HEPC | Q91au0 | hepatitis c |
| 998 | 74.5 | 6.2 | 156 | 2 | Q8KC46_CHLTE | Q8kc46 | chlorobium |
| 999 | 74 | 6.2 | 167 | 2 | Q81528_9HEPC | Q81528 | hepatitis c |
| 1000 | 74 | 6.2 | 173 | 2 | Q8WZ72_HUMAN | Q8wz72 | homo sapien |
| 1001 | 74 | 6.2 | 193 | 2 | Q5VHX0_EAV | Q5vhx0 | equine arte |
| 1002 | 74 | 6.2 | 220 | 2 | Q3ZSX9_PLAVI | Q3zsx9 | plasmodium |
| 1003 | 74 | 6.2 | 225 | 2 | Q5HCD2_EHRRW | Q5hcd2 | ehrlichia r |
| 1004 | 74 | 6.2 | 230 | 2 | Q91SA2_9CORO | Q91sa2 | coronavirus |
| 1005 | 74 | 6.2 | 231 | 1 | Q8Y70_LACPL | Q8y70 | lactobacill |
| 1006 | 74 | 6.2 | 231 | 2 | O27961_ARCFU | O27961 | archaeoglob |
| 1007 | 74 | 6.2 | 238 | 2 | O28892_ARCFU | O28892 | archaeoglob |
| 1008 | 74 | 6.2 | 249 | 2 | Q6HET1_BACHK | Q6het1 | bacillus th |
| 1009 | 74 | 6.2 | 255 | 2 | Q366H4_9GAMM | Q366h4 | shewanella |
| 1010 | 74 | 6.2 | 262 | 2 | Q66483_EAV | Q66483 | equine arte |
| 1011 | 74 | 6.2 | 278 | 2 | Q31RW0_SYN?7 | Q31rw0 | synechococc |
| 1012 | 74 | 6.2 | 279 | 2 | Q6CU18_KLULA | Q6cu18 | kluyveromyc |
| 1013 | 74 | 6.2 | 285 | 2 | Q4XPR5_PLACH | Q4xpr5 | plasmodium |
| 1014 | 74 | 6.2 | 286 | 1 | Q4E472_TRYCR | Q4e472 | trypanosoma |
| 1015 | 74 | 6.2 | 291 | 2 | P75058_MYCPN | P75058 | mycoplasma |
| 1016 | 74 | 6.2 | 291 | 2 | Q4AVT5_9BURK | Q4avt5 | polaromonas |
| 1017 | 74 | 6.2 | 295 | 2 | Q669G8_YERPS | Q669g8 | yersinia ps |
| 1018 | 74 | 6.2 | 295 | 1 | Q9WW5_PSEPU | Q9ww5 | pseudomonas |
| 1019 | 74 | 6.2 | 295 | 2 | Q6S4M3_PSEPU | Q6s4m3 | pseudomonas |
| 1020 | 74 | 6.2 | 297 | 2 | Q41Y2_KINRA | Q41y2 | kineococcus |
| 1021 | 74 | 6.2 | 300 | 1 | Q61BC3_CAEBR | Q61bc3 | caenorhabdi |
| 1022 | 74 | 6.2 | 309 | 2 | NU2M_ASCSU | P24877 | ascaris suu |
| 1023 | 74 | 6.2 | 312 | 2 | Q3DPI9_STRAG | Q3dpi9 | streptococc |
| 1024 | 74 | 6.2 | 312 | 2 | Q9YBD4_AERPE | Q9ybd4 | aeropyrum p |
| 1025 | 74 | 6.2 | 315 | 2 | Q9CH74_LACLA | Q9ch74 | lactococcus |
| 1026 | 74 | 6.2 | 321 | 2 | Q71O92_SPAEH | Q71o92 | spalax leuc |
| 1027 | 74 | 6.2 | 324 | 2 | Q8M6V0_9MAXI | Q8m6v0 | tigriopus j |
| 1028 | 74 | 6.2 | 330 | 2 | Q8DVZ6_STRMU | Q8dvz6 | streptococc |
| 1029 | 74 | 6.2 | 331 | 2 | Q3TU35_MOUSE | Q3tu35 | mus musculu |
| 1030 | 74 | 6.2 | 333 | 2 | Q3HOJ8_9ACTO | Q3hoj8 | nocardioide |
| 1031 | 74 | 6.2 | 339 | 2 | Q4FNS1_PELUB | Q4fns1 | pelagibacte |
| 1032 | 74 | 6.2 | 339 | 2 | Q61FG9_CAEBR | Q61fg9 | caenorhabdi |
| 1033 | 74 | 6.2 | 342 | 2 | Q62IV1_CAEBR | Q62iv1 | caenorhabdi |
| 1034 | 74 | 6.2 | 349 | 1 | 110R2_MOUSE | Q110r2 | mus musculu |
| 1035 | 74 | 6.2 | 350 | 2 | MTR1A_HUMAN | P48039 | homo sapien |
| 1036 | 74 | 6.2 | 351 | 2 | Q8VHM7_MOUSE | Q8vhm7 | mus musculu |
| 1037 | 74 | 6.2 | 354 | 2 | Q6SU34_MANSM | Q6su34 | mannheimia |
| 1038 | 74 | 6.2 | 357 | 2 | Q5FV66_MEDTR | Q5fv66 | medicago tr |
| 1039 | 74 | 6.2 | 359 | 2 | Q3ITR5_NATPD | Q3itr5 | natronomona |
| 1040 | 74 | 6.2 | 361 | 2 | Q64A19_9ARCH | Q64a19 | uncultured |
| 1041 | 74 | 6.2 | 372 | 2 | Q4CMV5_TRYCR | Q4cmv5 | trypanosoma |
| 1042 | 74 | 6.2 | 379 | 1 | CYB_THOMO | Q8wek2 | thomomys mo |
| 1043 | 74 | 6.2 | 379 | 2 | Q47980_THOBO | Q47980 | thomomys bo |
| 1044 | 74 | 6.2 | 379 | 2 | Q48022_THOMO | Q48022 | thomomys mo |
| 1045 | 74 | 6.2 | 379 | 2 | Q48003_THOMO | Q48003 | thomomys mo |
| 1046 | 74 | 6.2 | 379 | 2 | Q59J17_9SCIU | Q59j17 | peromys vo |
| 1047 | 74 | 6.2 | 379 | 2 | Q8HH17_THOBO | Q8hh17 | thomomys bo |
| 1048 | 74 | 6.2 | 380 | 1 | Q8WEK5_THOTA | Q8wek5 | thomomys ta |
| 1049 | 74 | 6.2 | 381 | 1 | CYB_PSENI | Q8hij7 | pseudantech |
| 1050 | 74 | 6.2 | 382 | 2 | Q5R7A1_PONPY | Q5r7a1 | pongo pygma |
| 1051 | 74 | 6.2 | 396 | 2 | Q2YWW7_STAAB | Q2yww7 | staphylococ |
| 1052 | 74 | 6.2 | 396 | 2 | Q6GAR1_STAAS | Q6gar1 | staphylococ |
| 1053 | 74 | 6.2 | 396 | 2 | Q6GI68_STAAR | Q6gi68 | staphylococ |
| 1054 | 74 | 6.2 | 396 | 2 | Q7A6D3_STAAN | Q7a6d3 | staphylococ |
| 1055 | 74 | 6.2 | 396 | 2 | Q8NXC4_STAAW | Q8nxc4 | staphylococ |
| 1056 | 74 | 6.2 | 396 | 2 | Q99W76_STAAM | Q99w76 | staphylococ |
| 1057 | 74 | 6.2 | 397 | 2 | Q5HH70_STAAC | Q5hh70 | staphylococ |
| 1058 | 74 | 6.2 | 398 | 2 | Q42254_PLABE | Q42254 | plasmodium |
| 1059 | 74 | 6.2 | 398 | 2 | Q2PQV8_9NOCA | Q2pqv8 | rhodococcus |
| 1060 | 74 | 6.2 | 406 | 2 | Q5NEU8_FRATT | Q5neu8 | francisella |
| 1061 | 74 | 6.2 | 410 | 2 | Q3F83_9BURK | Q3f83 | burkholderi |
| 1062 | 74 | 6.2 | 418 | 2 | Q4R103_TETNG | Q4r103 | tetraodon n |
| 1063 | 74 | 6.2 | 418 | 2 | Q6QFB9_LEGPN | Q6qfb9 | legionella |
| 1064 | 73.5 | 6.2 | 418 | 2 | Q6QCS_LEGPN | Q6qcs | legionella |
| 1065 | 73.5 | 6.2 | 436 | 2 | Q5QZG8_IDILO | Q5qzg8 | idiomarina |
| 1066 | 73.5 | 6.2 | 442 | 2 | Q9CEG6_LACLA | Q9ceg6 | lactococcus |
| 1067 | 73.5 | 6.2 | 452 | 2 | Q2S5B2_9GAMM | Q2s5b2 | shewanella |
| 1068 | 73.5 | 6.2 | 452 | 2 | Q4NJC7_9MICC | Q4njc7 | arthrobacte |
| 1069 | 73.5 | 6.2 | 457 | 2 | Q8RB27_THETN | Q8rb27 | thermoanaer |
| 1070 | 73.5 | 6.2 | 459 | 2 | Q39U36_GEOMG | Q39u36 | geobacter m |
| 1071 | 73.5 | 6.2 | 475 | 2 | Q9S2G7_STRCO | Q9s2g7 | streptomyce |
| 1072 | 73.5 | 6.2 | 481 | 2 | Q4Q1F4_LEIMA | Q4q1f4 | leishmania |
| 1073 | 73.5 | 6.2 | 485 | 2 | Q9XVK0_CAEEL | Q9xvk0 | caenorhabdi |
| 1074 | 73.5 | 6.2 | 487 | 2 | O23384_ARATH | O23384 | arabidopsis |
| 1075 | 73.5 | 6.2 | 493 | 2 | Q9EVJ7_FLAJU | Q9evj7 | flavobacter |
| 1076 | 73.5 | 6.2 | 503 | 2 | Q6M052_METMP | Q6m052 | methanococc |
| 1077 | 73.5 | 6.2 | 505 | 2 | Q2IKZ1_9DELT | Q2ikz1 | anaeromyxob |
| 1078 | 73.5 | 6.2 | 528 | 2 | Q70IQ9_KLULA | Q70iq9 | kluyveromyc |
| 1079 | 73.5 | 6.2 | 530 | 2 | Q41S60_FERAC | Q41s60 | ferroplasma |
| 1080 | 73.5 | 6.2 | 530 | 2 | Q51FL8_ENTHI | Q51fl8 | entamoeba h |
| 1081 | 73.5 | 6.2 | 530 | 2 | Q51FL8_ENTHI | Q51fl8 | entamoeba h |
| 1082 | 73.5 | 6.2 | 581 | 2 | Q6FI16_CANGA | Q6fi16 | candida gla |
| 1083 | 73.5 | 6.2 | 581 | 2 | Q6FI33_CANGA | Q6fi33 | candida gla |
| 1084 | 73.5 | 6.2 | 584 | 2 | Q5KA08_CRYNE | Q5ka08 | cryptococcu |
| 1085 | 73.5 | 6.2 | 587 | 2 | Q5KA09_CRYNE | Q5ka09 | cryptococcu |
| 1086 | 73.5 | 6.2 | 599 | 2 | Q37RO8_SPHAR | Q37ro8 | solibacter |
| 1087 | 73.5 | 6.2 | 650 | 2 | Q9S6S6_9LACT | Q9s6s6 | lactococcus |
| 1088 | 73.5 | 6.2 | 681 | 2 | Q4FTS7_PSYAR | Q4fts7 | psychrobact |
| 1089 | 73.5 | 6.2 | 689 | 2 | Q6FNV6_CANGA | Q6fnv6 | candida gla |
| 1090 | 73.5 | 6.2 | 742 | 2 | Q43QW4_SOLUS | Q43qw4 | solibacter |
| 1091 | 73.5 | 6.2 | 841 | 2 | Q9AIP1_CARRU | Q9aip1 | carsonella |
| 1092 | 73.5 | 6.2 | 846 | 2 | Q93U47_CARRU | Q93u47 | carsonella |
| 1093 | 73.5 | 6.2 | 892 | 2 | Q8TGB2_CANAL | Q8tgb2 | candida alb |
| 1094 | 74 | 6.2 | 943 | 2 | Q4IMI9_GIBZE | Q4imi9 | gibberella |
| 1095 | 74 | 6.2 | 1123 | 2 | Q9SE99_ARATH | Q9se99 | arabidopsis |
| 1096 | 74 | 6.2 | 1123 | 2 | Q9SPU7_ARATH | Q9spu7 | arabidopsis |
| 1097 | 74 | 6.2 | 1152 | 2 | Q5S1S2_CRYNE | Q5s1s2 | cryptococcu |
| 1098 | 74 | 6.2 | 1216 | 2 | Q5KCX7_CRYNE | Q5kcx7 | cryptococcu |
| 1099 | 74 | 6.2 | 1216 | 2 | Q913V3_9HEPC | Q913v3 | hepatitis c |
| 1100 | 74 | 6.2 | 3010 | 2 | Q9DTE8_9HEPC | Q9dte8 | hepatitis c |
| 1101 | 74 | 6.2 | 3010 | 2 | Q9J3H6_9HEPC | Q9j3h6 | hepatitis c |
| 1102 | 74 | 6.2 | 3010 | 2 | Q9QIY1_9HEPC | Q9qiy1 | hepatitis c |
| 1103 | 74 | 6.2 | 3010 | 2 | Q9QIY2_9HEPC | Q9qiy2 | hepatitis c |
| 1104 | 73.5 | 6.2 | 120 | 2 | Q9SKA6_ARATH | Q9ska6 | arabidopsis |
| 1105 | 73.5 | 6.2 | 153 | 2 | Q92XD3_RHIME | Q92xd3 | rhizobium m |
| 1106 | 73.5 | 6.2 | 174 | 2 | Q2NGT7_9EURY | Q2ngt7 | methanosph |
| 1107 | 73.5 | 6.2 | 180 | 2 | Q82XS3_PYRAE | Q82xs3 | pyrobaculum |
| 1108 | 73.5 | 6.2 | 180 | 2 | P71251_ECOLI | P71251 | escherichia |
| 1109 | 73.5 | 6.2 | 180 | 2 | P71257_ECOLI | P71257 | escherichia |
| 1110 | 73.5 | 6.2 | 199 | 2 | P75018_ECOLI | P75018 | escherichia |
| 1111 | 73.5 | 6.2 | 216 | 1 | Y203_AQUAE | Y203 | aquifex aeo |
| 1112 | 73.5 | 6.2 | 217 | 2 | Q4TEY9_TETNG | Q4tey9 | tetraodon n |
| 1113 | 73.5 | 6.2 | 226 | 2 | Q5MAP0_9CORO | Q5map0 | coronavirus |
| 1114 | 73.5 | 6.2 | 226 | 2 | Q9J0X1_9CORO | Q9j0x1 | infectious |
| 1115 | 73.5 | 6.2 | 246 | 2 | Q4D4K9_TRYCR | Q4d4k9 | trypanosoma |
| 1116 | 73.5 | 6.2 | 246 | 2 | Q50Z61_ENTHI | Q50z61 | entamoeba h |
| 1117 | 73.5 | 6.2 | 267 | 2 | Q8HBP0_PERLO | Q8hbp0 | perognathus |
| 1118 | 73.5 | 6.2 | 270 | 2 | Q8HIY6_PERLO | Q8hiy6 | perognathus |
| 1119 | 73.5 | 6.2 | 270 | 2 | Q95L51_CAPHI | Q95l51 | capra hircu |
| 1120 | 73.5 | 6.2 | 274 | 2 | Q4JC08_SULAC | Q4jc08 | sulfolobus |
| 1121 | 73.5 | 6.2 | 278 | 2 | Q3NNI2_SHEFR | Q3nni2 | shewanella |
| 1122 | 73.5 | 6.2 | 281 | 2 | Q2SQF4_9GAMM | Q2sqf4 | hahella che |
| 1123 | 73.5 | 6.2 | 281 | 2 | Q4HSI6_CAMUP | Q4hsi6 | campylobact |
| 1124 | 73.5 | 6.2 | 298 | 2 | Q6Z2T3_ORYSA | Q6z2t3 | oryza sativ |
| 1125 | 73.5 | 6.2 | 298 | 2 | Q6Z2T3_ORYSA | Q6z2t3 | oryza sativ |
| 1126 | 73.5 | 6.2 | 303 | 2 | Q5J3K6_RAT | Q5j3k6 | rattus norv |

| No. | | | Len | N | Accession | Organism |
|---|---|---|---|---|---|---|
| 1127 | 73.5 | 6.2 | 304 | 2 | Q2RIE6_MOOTH | moorella th |
| 1128 | 73.5 | 6.2 | 304 | 2 | Q5NP42_ZYMMO | zymomonas m |
| 1129 | 73.5 | 6.2 | 305 | 2 | Q4P0E6_USTMA | ustilago ma |
| 1130 | 73.5 | 6.2 | 306 | 2 | Q37MI0_RHOPA | rhodopseudo |
| 1131 | 73.5 | 6.2 | 307 | 2 | Q2IYA5_RHOPA | rhodopseudo |
| 1132 | 73.5 | 6.2 | 316 | 2 | Q3AQX9_CHLCH | chlorobium |
| 1133 | 73.5 | 6.2 | 318 | 2 | Q58895_SYNY3 | synechocyst |
| 1134 | 73.5 | 6.2 | 338 | 1 | P37520_BACSU | bacillus su |
| 1135 | 73.5 | 6.2 | 355 | 2 | Q4J826_SULAC | sulfolobus |
| 1136 | 73.5 | 6.2 | 359 | 2 | Q2NTQ3_SODGL | sodalis glo |
| 1137 | 73.5 | 6.2 | 360 | 2 | Q8UUW8_BRARE | brachydanio |
| 1138 | 73.5 | 6.2 | 367 | 2 | Q64BD6_9ARCH | uncultured |
| 1139 | 73.5 | 6.2 | 373 | 2 | Q5FI17_LACAC | lactobacill |
| 1140 | 73.5 | 6.2 | 379 | 1 | CYB_PHOGR | phoca groen |
| 1141 | 73.5 | 6.2 | 379 | 1 | CYB_THOTA | thomomys ta |
| 1142 | 73.5 | 6.2 | 379 | 2 | Q9G3M8_OCHCU | ochotona cu |
| 1143 | 73.5 | 6.2 | 379 | 2 | Q9G3M8_9RODE | perognathus |
| 1144 | 73.5 | 6.2 | 379 | 2 | Q50BJ0_9RODE | perognathus |
| 1145 | 73.5 | 6.2 | 379 | 2 | Q50BJ7_PERPA | perognathus |
| 1146 | 73.5 | 6.2 | 379 | 2 | Q588N6_SCILI | sciurus lis |
| 1147 | 73.5 | 6.2 | 380 | 1 | Q2N2B6_PERFA | perognathus |
| 1148 | 73.5 | 6.2 | 384 | 1 | CYB_PERFA | perognathus |
| 1149 | 73.5 | 6.2 | 384 | 1 | P15547_STRPU | strongyloce |
| 1150 | 73.5 | 6.2 | 385 | 2 | Q8Z719_SALTI | salmonella |
| 1151 | 73.5 | 6.2 | 387 | 2 | OPGC_SALTY | salmonella |
| 1152 | 73.5 | 6.2 | 387 | 2 | OPGC_SALTI | salmonella |
| 1153 | 73.5 | 6.2 | 389 | 1 | P94442_BACSU | bacillus su |
| 1154 | 73.5 | 6.2 | 391 | 1 | Q9KWU2_9SPHN | sphingomona |
| 1155 | 73.5 | 6.2 | 397 | 2 | Q7MVX5_PORGI | porphyromon |
| 1156 | 73.5 | 6.2 | 398 | 2 | OXYR_MACMU | macaca mula |
| 1157 | 73.5 | 6.2 | 409 | 2 | OXYR_BOVIN | bos taurus |
| 1158 | 73.5 | 6.2 | 413 | 2 | Q82ZF7_ENTFA | enterococcu |
| 1159 | 73.5 | 6.2 | 421 | 2 | Q82QZ7_ENTFA | enterococcu |
| 1160 | 73.5 | 6.2 | 425 | 2 | Q3CNW3_ALTAT | pseudoalter |
| 1161 | 73.5 | 6.2 | 435 | 2 | Q7V140_PROMP | prochloroco |
| 1162 | 73.5 | 6.2 | 442 | 2 | Q928T3_LISIN | listeria in |
| 1163 | 73.5 | 6.2 | 442 | 2 | Q8PK37_XANAC | xanthomonas |
| 1164 | 73.5 | 6.2 | 451 | 2 | Q6D6K1_ERWCT | erwinia car |
| 1165 | 73.5 | 6.2 | 470 | 2 | Q48IN0_COLP3 | colwellia p |
| 1166 | 73.5 | 6.2 | 491 | 1 | Q8GZ34_ARATH | arabidopsis |
| 1167 | 73.5 | 6.2 | 491 | 2 | Q9XIQ7_ARATH | arabidopsis |
| 1168 | 73.5 | 6.2 | 518 | 2 | Q4E247_TRYCR | trypanosoma |
| 1169 | 73.5 | 6.2 | 523 | 2 | Q36Q01_MARHY | marinobacte |
| 1170 | 73.5 | 6.2 | 542 | 2 | VIE1_HCMVA | human cytom |
| 1171 | 73.5 | 6.2 | 555 | 2 | P13202_HCMV | human cytom |
| 1172 | 73.5 | 6.2 | 557 | 2 | Q6SW28_HCMV | human cytom |
| 1173 | 73.5 | 6.2 | 563 | 2 | Q7RT44_PLAVO | plasmodium |
| 1174 | 73.5 | 6.2 | 570 | 2 | Q64WY6_BACFN | bacteroides |
| 1175 | 73.5 | 6.2 | 574 | 2 | Q5LG29_BACTN | bacteroides |
| 1176 | 73.5 | 6.2 | 574 | 2 | Q7PFV1_ANOGA | anopheles g |
| 1177 | 73.5 | 6.2 | 607 | 2 | Q8VZE2_ARATH | arabidopsis |
| 1178 | 73.5 | 6.2 | 614 | 2 | Q5ATP6_EMENI | aspergillus |
| 1179 | 73.5 | 6.2 | 634 | 1 | Q3N230_9DELT | syntrophoba |
| 1180 | 73.5 | 6.2 | 634 | 2 | Q93990_CANAL | candida alb |
| 1181 | 73.5 | 6.2 | 634 | 2 | Q3N230_9DELT | candida alb |
| 1182 | 73.5 | 6.2 | 637 | 1 | Q5AP9_CANAL | candida alb |
| 1183 | 73.5 | 6.2 | 640 | 1 | Q6DFJ5_XENLA | xenopus lae |
| 1184 | 73.5 | 6.2 | 641 | 2 | Q5CE41_CRYHO | cryptospori |
| 1185 | 73.5 | 6.2 | 653 | 2 | Q9PC78_XYLFA | xylella fas |
| 1186 | 73.5 | 6.2 | 661 | 2 | Q3R3X0_XYLFA | xylella fas |
| 1187 | 73.5 | 6.2 | 715 | 2 | Q3REM6_XYLFA | xylella fas |
| 1188 | 73.5 | 6.2 | 731 | 1 | MUTL_BACHD | bacillus ha |
| 1189 | 73.5 | 6.2 | 846 | 2 | APRN_ENTHI | entamoeba h |
| 1190 | 73.5 | 6.2 | 859 | 2 | P20301_ENTHI | entamoeba h |
| 1191 | 73.5 | 6.2 | 881 | 2 | Q3NCP3_9PROT | nitrosomona |
| 1192 | 73.5 | 6.2 | 992 | 2 | Q8TTHI_METAC | methanosarc |
| 1193 | 73.5 | 6.2 | 1006 | 2 | O68468_CORAM | corynebacte |
| 1194 | 73.5 | 6.2 | 1019 | 2 | O16531_CAEEL | glyceria gr |
| 1195 | 73.5 | 6.2 | 1049 | 2 | Q51315_ENTHI | caenorhabdi |
| 1196 | 73.5 | 6.2 | 1095 | 2 | Q4YH96_PLABE | plasmodium |
| 1197 | 73.5 | 6.2 | 1100 | 2 | Q2KG26_MAGGR | magnaporthe |
| 1198 | 73.5 | 6.2 | 1174 | 2 | Q36ND8_MARHY | marinobacte |
| 1199 | 73.5 | 6.2 | 1175 | 2 | Q7MOO6_9CORO | murine hepa |

| No. | | | Len | N | Accession | Organism |
|---|---|---|---|---|---|---|
| 1200 | 73.5 | 6.2 | 1277 | 2 | Q76G00_CIOIN | ciona intes |
| 1201 | 73.5 | 6.2 | 1287 | 2 | Q7YU59_DROME | drosophila |
| 1202 | 73.5 | 6.2 | 1287 | 2 | Q9U5W1_DROME | drosophila |
| 1203 | 73.5 | 6.2 | 1292 | 2 | Q9V124_DROME | drosophila |
| 1204 | 73.5 | 6.2 | 1292 | 2 | Q9AIH0_CARRU | carsonella |
| 1205 | 73.5 | 6.2 | 1476 | 2 | Q96SD3_DICDI | dictyosteli |
| 1206 | 73.5 | 6.2 | 1545 | 2 | Q8GU65_ORYSA | oryza sativ |
| 1207 | 73.5 | 6.2 | 2666 | 2 | Q6FW99_CANGA | candida gla |
| 1208 | 73.5 | 6.2 | 3007 | 2 | Q4SSR8_TETNG | tetraodon n |
| 1209 | 73.5 | 6.2 | 3010 | 2 | Q9DTE6_9HEPC | hepatitis c |
| 1210 | 73.5 | 6.2 | 3381 | 2 | Q8IDK4_PLAF7 | plasmodium |
| 1211 | 73.5 | 6.2 | 4470 | 2 | Q66WN5_9CORO | murine hepa |
| 1212 | 73.5 | 6.2 | 4839 | 2 | Q2N3S8_POLCB | polyangium |
| 1213 | 73.5 | 6.2 | 7176 | 1 | RIAB_CVMA5 | m replicase |
| 1214 | 73.5 | 6.2 | 7176 | 1 | P16342_CVMA5 | m replicase |
| 1215 | 73 | 6.2 | 114 | 2 | Q66WN6_9CORO | murine hepa |
| 1216 | 73 | 6.2 | 114 | 1 | Q75XA7_HELPY | helicobacte |
| 1217 | 73 | 6.2 | 138 | 2 | Q9ZLU2_HELPJ | helicobacte |
| 1218 | 73 | 6.1 | 138 | 2 | Q97777_ELEMA | elephas max |
| 1219 | 73 | 6.1 | 140 | 2 | Q37328_RHOPA | rhodopseudo |
| 1220 | 73 | 6.1 | 145 | 2 | Q64145_MURI | ratus sp. |
| 1221 | 73 | 6.1 | 155 | 2 | Q9UXB0_SULSO | sulfolobus |
| 1222 | 73 | 6.1 | 155 | 2 | Q7VJP1_HELHP | helicobacte |
| 1223 | 73 | 6.1 | 156 | 2 | Q81510_9HEPC | hepatitis c |
| 1224 | 73 | 6.1 | 156 | 2 | Q81522_9HEPC | hepatitis c |
| 1225 | 73 | 6.1 | 163 | 2 | Q81537_9HEPC | hepatitis c |
| 1226 | 73 | 6.1 | 220 | 2 | Q80RY8_9HEPC | hepatitis c |
| 1227 | 73 | 6.1 | 223 | 2 | Q72Z40_BACC1 | bacillus ce |
| 1228 | 73 | 6.1 | 223 | 2 | VME1_IBVG | avian infec |
| 1229 | 73 | 6.1 | 226 | 2 | Q91S97_9CORO | infectious |
| 1230 | 73 | 6.1 | 238 | 2 | Q7T9P6_9CORO | infectious |
| 1231 | 73 | 6.1 | 238 | 1 | PYRF_BACCR | bacillus ce |
| 1232 | 73 | 6.1 | 238 | 2 | Q4MJ45_BACCE | bacillus ce |
| 1233 | 73 | 6.1 | 238 | 2 | Q636E3_BACCZ | bacillus ce |
| 1234 | 73 | 6.1 | 249 | 2 | Q73216_BACC1 | bacillus ce |
| 1235 | 73 | 6.1 | 249 | 2 | Q362R1_BACC1 | shewanella |
| 1236 | 73 | 6.1 | 249 | 2 | Q48TQ7_STRPM | streptococc |
| 1237 | 73 | 6.1 | 249 | 2 | Q48TG7_STRPM | streptococc |
| 1238 | 73 | 6.1 | 255 | 2 | Q7DAL8_STRP1 | streptococc |
| 1239 | 73 | 6.1 | 255 | 2 | Q9FDU6_STRPY | streptococc |
| 1240 | 73 | 6.1 | 264 | 2 | P87639_EAV | equine arte |
| 1241 | 73 | 6.1 | 264 | 2 | Q9YNU0_EAV | equine arte |
| 1242 | 73 | 6.1 | 264 | 2 | Q9QN39_ANOGA | anopheles g |
| 1243 | 73 | 6.1 | 269 | 2 | Q8DAQ9_VIBVU | vibrio vuln |
| 1244 | 73 | 6.1 | 269 | 2 | Q8DT98_MARHY | marinobacte |
| 1245 | 73 | 6.1 | 273 | 2 | Q36T98_MARHY | thiomicrosp |
| 1246 | 73 | 6.1 | 279 | 2 | Q30RA4_THIDN | rhizobium e |
| 1247 | 73 | 6.1 | 282 | 1 | Q2K662_RHIET | xiphinema a |
| 1248 | 73 | 6.1 | 290 | 2 | NU2M_CAEEL | caenorhabdi |
| 1249 | 73 | 6.1 | 290 | 2 | Q5HGI3_STAAC | staphylococ |
| 1250 | 73 | 6.1 | 290 | 2 | Q6G9W4_STAAS | staphylococ |
| 1251 | 73 | 6.1 | 294 | 2 | Q8NX00_STAAW | staphylococ |
| 1252 | 73 | 6.1 | 295 | 2 | Q5AZG6_EMENI | aspergillus |
| 1253 | 73 | 6.1 | 295 | 2 | Q4X7M3_PLACH | plasmodium |
| 1254 | 73 | 6.1 | 295 | 2 | Q8VUQ2_PSEPU | pseudomonas |
| 1255 | 73 | 6.1 | 295 | 2 | Q8VUQ2_PSEPU | pseudomonas |
| 1256 | 73 | 6.1 | 295 | 2 | Q88PN3_PSEPK | pseudomonas |
| 1257 | 73 | 6.1 | 303 | 2 | Q94E0_ARATH | arabidopsis |
| 1258 | 73 | 6.1 | 314 | 2 | Q8ESH3_OCEIH | oceanobacil |
| 1259 | 73 | 6.1 | 315 | 1 | Q99NR7_MUSAV | muscardiniu |
| 1260 | 73 | 6.1 | 319 | 2 | Q9H6T9_HUMAN | homo sapien |
| 1261 | 73 | 6.1 | 326 | 2 | Q2KDV3_RHIET | rhizobium e |
| 1262 | 73 | 6.1 | 326 | 2 | Q94EJ0_ARATH | rhizobium e |
| 1263 | 73 | 6.1 | 335 | 2 | P54129_ENCCU | encephalito |
| 1264 | 73 | 6.1 | 335 | 1 | SRG7_CAEEL | caenorhabdi |
| 1265 | 73 | 6.1 | 340 | 2 | Q9N2T2_CAEEL | caenorhabdi |
| 1266 | 73 | 6.1 | 343 | 2 | Q7YFU0_9HYME | caenorhabdi |
| 1267 | 73 | 6.1 | 343 | 2 | Q85AS7_UMASC | uma scopari |
| 1268 | 73 | 6.1 | 348 | 2 | Q9TD49_9HYME | cynoleblas |
| 1269 | 73 | 6.1 | 358 | 1 | GHSR_MOUSE | mus musculu |
| 1270 | 73 | 6.1 | 364 | 1 | Q4E9M7_9RICK | wolbachia e |
| 1271 | 73 | 6.1 | 364 | 1 | GHSR_RAT | rattus norv |
| 1272 | 73 | 6.1 | 375 | 2 | Q86NC0_CAEEL | caenorhabdi |

Left column block:

| No. | Score | | Len | F | Accession | ID | Organism |
|---|---|---|---|---|---|---|---|
| 1273 | 73 | 6.1 | 378 | 2 | Q70EG4_9RODE | q70eg4 | saccostomus |
| 1274 | 73 | 6.1 | 378 | 2 | Q70EG5_9RODE | q70eg5 | saccostomus |
| 1275 | 73 | 6.1 | 379 | 1 | CYB_CRAFU | cyb | cratogeomys |
| 1276 | 73 | 6.1 | 379 | 2 | Q34099_CRAFU | q34099 | cratogeomys |
| 1277 | 73 | 6.1 | 379 | 2 | Q698Q2_CRAFU | q698q2 | cratogeomys |
| 1278 | 73 | 6.1 | 383 | 2 | Q8WDV7_CRATY | q8wdv7 | cratogeomys |
| 1279 | 73 | 6.1 | 391 | 2 | Q9GL20_CYNSP | q9gl20 | cynopterus |
| 1280 | 73 | 6.1 | 394 | 1 | Y450_BUCAP | y450 | buchnera ap |
| 1281 | 73 | 6.1 | 396 | 2 | Q6EE99_LATCH | q6ee99 | latimeria c |
| 1282 | 73 | 6.1 | 396 | 2 | Q3F4A7_9BURK | q3f4a7 | burkholderi |
| 1283 | 73 | 6.1 | 396 | 2 | Q44YS3_9BURK | q44ys3 | burkholderi |
| 1284 | 73 | 6.1 | 399 | 2 | Q39KD3_BURS3 | q39kd3 | burkholderi |
| 1285 | 73 | 6.1 | 401 | 2 | Q61OJ3_PICTO | q61oj3 | picrophilus |
| 1286 | 73 | 6.1 | 401 | 2 | Q6KZX3_PICTO | q6kzx3 | picrophilus |
| 1287 | 73 | 6.1 | 412 | 2 | Q34D58_RHOPA | q34d58 | rhodopseudo |
| 1288 | 73 | 6.1 | 414 | 2 | Q61M38_CASER | q61m38 | caenorhabdi |
| 1289 | 73 | 6.1 | 424 | 2 | Q31S50_NATPD | q31s50 | natronomona |
| 1290 | 73 | 6.1 | 437 | 2 | Q3AVM8_SYNS9 | q3avm8 | synechococc |
| 1291 | 73 | 6.1 | 446 | 2 | Q4YN50_PLABE | q4yn50 | plasmodium |
| 1292 | 73 | 6.1 | 450 | 2 | Q8H9B3_BRACM | q8h9b3 | brassica ca |
| 1293 | 73 | 6.1 | 450 | 1 | VGLM_EHV1B | vglm | equine herp |
| 1294 | 73 | 6.1 | 452 | 2 | Q6S6V2_9ALPH | q6s6v2 | equid herpe |
| 1295 | 73 | 6.1 | 453 | 2 | Q36010_9GAMM | q36010 | shewanella |
| 1296 | 73 | 6.1 | 461 | 2 | Q94307_CAEEL | q94307 | caenorhabdi |
| 1297 | 73 | 6.1 | 461 | 2 | Q4K0J6_STRPN | q4k0j6 | streptococc |
| 1298 | 73 | 6.1 | 470 | 2 | Q9R923_STRPN | q9r923 | streptococc |
| 1299 | 73 | 6.1 | 474 | 2 | Q54PF0_DICDI | q54pf0 | dictyosteli |
| 1300 | 73 | 6.1 | 481 | 2 | Q94CI7_ARATH | q94ci7 | arabidopsis |
| 1301 | 73 | 6.1 | 487 | 2 | Q4K4Z1_PSEF5 | q4k4z1 | pseudomonas |
| 1302 | 73 | 6.1 | 487 | 2 | Q37NN7_RHOPA | q37nn7 | rhodopseudo |
| 1303 | 73 | 6.1 | 488 | 2 | Q7MBA5_PHOLL | q7mba5 | photorhabdu |
| 1304 | 73 | 6.1 | 494 | 2 | Q4HRT1_CAMUP | q4hrt1 | campylobact |
| 1305 | 73 | 6.1 | 494 | 2 | Q9J3M0_HUMAN | q9j3m0 | homo sapien |
| 1306 | 73 | 6.1 | 509 | 1 | KCNF1_HUMAN | kcnf1 | homo sapien |
| 1307 | 73 | 6.1 | 510 | 2 | Q5CUK7_CRYPV | q5cuk7 | cryptospori |
| 1308 | 73 | 6.1 | 520 | 2 | Q27072_TAESO | q27072 | taenia soli |
| 1309 | 73 | 6.1 | 525 | 2 | Q5KWR7_GEOKA | q5kwr7 | geobacillus |
| 1310 | 73 | 6.1 | 546 | 2 | Q44MH7_CHLLI | q44mh7 | chlorobium |
| 1311 | 73 | 6.1 | 553 | 2 | Q5EAY8_XENLA | q5eay8 | xenopus lae |
| 1312 | 73 | 6.1 | 553 | 2 | Q3MP12_CANAL | q3mp12 | candida alb |
| 1313 | 73 | 6.1 | 553 | 2 | Q59PN9_CANAL | q59pn9 | candida alb |
| 1314 | 73 | 6.1 | 556 | 2 | Q9ZJ35_HELPJ | q9zj35 | helicobacte |
| 1315 | 73 | 6.1 | 597 | 2 | Q7QZJ9_GIALA | q7qzj9 | giardia lam |
| 1316 | 73 | 6.1 | 599 | 2 | Q2SRQ8_MYCCA | q2srq8 | mycoplasma |
| 1317 | 73 | 6.1 | 599 | 2 | Q3Y0F7_ENTFC | q3y0f7 | enterococcu |
| 1318 | 73 | 6.1 | 604 | 2 | Q3V5J8_CAEEL | q3v5j8 | caenorhabdi |
| 1319 | 73 | 6.1 | 616 | 2 | Q6BIQ1_DEBHA | q6biq1 | debaryomyce |
| 1320 | 73 | 6.1 | 623 | 2 | Q4RMH4_TETNG | q4rmh4 | tetraodon n |
| 1321 | 73 | 6.1 | 635 | 2 | Q86X77_HUMAN | q86x77 | homo sapien |
| 1322 | 73 | 6.1 | 643 | 2 | Q7NBK6_MYCGA | q7nbk6 | mycoplasma |
| 1323 | 73 | 6.1 | 668 | 2 | Q9ALX8_BURPS | q9alx8 | burkholderi |
| 1324 | 73 | 6.1 | 668 | 2 | Q63L6I_BURPS | q63l6i | burkholderi |
| 1325 | 73 | 6.1 | 676 | 2 | Q9VF31_DROME | q9vf31 | drosophila |
| 1326 | 73 | 6.1 | 676 | 2 | Q2WL35_CLOBE | q2wl35 | clostridium |
| 1327 | 73 | 6.1 | 703 | 2 | Q4W5R5_CAEEL | q4w5r5 | caenorhabdi |
| 1328 | 73 | 6.1 | 716 | 2 | Q59LX3_CANAL | q59lx3 | candida alb |
| 1329 | 73 | 6.1 | 788 | 1 | P64155_STAAC | p64155 | staphylococ |
| 1330 | 73 | 6.1 | 788 | 1 | P64154_STAAM | p64154 | staphylococ |
| 1331 | 73 | 6.1 | 788 | 1 | FTSK_STAAN | ftsk | staphylococ |
| 1332 | 73 | 6.1 | 789 | 2 | FTSK_STAAC | ftsk | staphylococ |
| 1333 | 73 | 6.1 | 789 | 1 | FTSK_STAAR | ftsk | staphylococ |
| 1334 | 73 | 6.1 | 806 | 2 | Q5Z6J8_ORYSA | q5z6j8 | oryza sativ |
| 1335 | 73 | 6.1 | 832 | 2 | Q5Z618_ORYSA | q5z618 | oryza sativ |
| 1336 | 73 | 6.1 | 844 | 2 | Q7UQF9_RHOBA | q7uqf9 | rhodopirell |
| 1337 | 73 | 6.1 | 861 | 2 | Q6KY8_PICTO | q6ky8 | picrophilus |
| 1338 | 73 | 6.1 | 861 | 1 | Q4DIL4_TRYCR | q4dil4 | trypanosoma |
| 1339 | 73 | 6.1 | 966 | 2 | Q9AVX8_GUITH | q9avx8 | guillardia |
| 1340 | 73 | 6.1 | 966 | 1 | PKD2_MOUSE | pkd2 | mus musculu |
| 1341 | 73 | 6.1 | 966 | 2 | Q7TSI7_MOUSE | q7tsi7 | mus musculu |
| 1342 | 73 | 6.1 | 971 | 2 | Q8BPR6_MOUSE | q8bpr6 | mus musculu |
| 1343 | 73 | 6.1 | 1035 | 2 | O60337_HUMAN | o60337 | homo sapien |
| 1344 | 73 | 6.1 | 1052 | 2 | Q967W1_SCHMA | q967w1 | schistosoma |
| 1344 | 73 | 6.1 | 1075 | 2 | Q41D65_9BACI | q41d65 | exiguobacte |
| 1345 | 73 | 6.1 | 1075 | 2 | Q9LPE2_ARATH | q9lpe2 | arabidopsis |
| 1345 | 73 | 6.1 | 1111 | 2 | Q86FP2_CAEEL | q86fp2 | caenorhabd |

Right column block:

| No. | Score | | Len | F | Accession | ID | Organism |
|---|---|---|---|---|---|---|---|
| 1346 | 73 | 6.1 | 1127 | 2 | Q9N323_CAEEL | q9n323 | caenorhabdi |
| 1347 | 73 | 6.1 | 1156 | 2 | Q4WGM4_ASPFU | q4wgm4 | aspergillus |
| 1348 | 73 | 6.1 | 1268 | 2 | Q55375_DICDI | q55375 | dictyosteli |
| 1349 | 73 | 6.1 | 1931 | 2 | Q8RJY3_STIAU | q8rjy3 | stigmatella |
| 1350 | 73 | 6.1 | 1951 | 2 | Q7P2N7_ANOGA | q7p2n7 | anopheles g |
| 1351 | 73 | 6.1 | 3010 | 2 | P88803_9HEPC | p88803 | hepatitis c |
| 1352 | 73 | 6.1 | 3010 | 2 | Q9J3G1_9HEPC | q9j3g1 | hepatitis c |
| 1353 | 73 | 6.1 | 3010 | 2 | Q9J3I0_9HEPC | q9j3i0 | hepatitis c |
| 1354 | 73 | 6.1 | 3013 | 2 | Q9QIX9_9HEPC | q9qix9 | hepatitis c |
| 1355 | 73 | 6.1 | 3013 | 2 | Q9QIY0_9HEPC | q9qiy0 | hepatitis c |
| 1356 | 73 | 6.1 | 6875 | 2 | Q28733_RABIT | q28733 | oryctolagus |
| 1357 | 72.5 | 6.1 | 105 | 2 | Q5ALK7_CANAL | q5alk7 | candida alb |
| 1358 | 72.5 | 6.1 | 144 | 2 | Q2LWL0_9DELT | q2lwl0 | syntrophus |
| 1359 | 72.5 | 6.1 | 156 | 2 | Q81S16_9HEPC | q81s16 | hepatitis c |
| 1360 | 72.5 | 6.1 | 156 | 2 | Q81S19_9HEPC | q81s19 | hepatitis c |
| 1361 | 72.5 | 6.1 | 167 | 2 | Q5KIU4_CRYNE | q5kiu4 | cryptococcu |
| 1362 | 72.5 | 6.1 | 170 | 2 | Q2ULP6_ASPOR | q2ulp6 | aspergillus |
| 1363 | 72.5 | 6.1 | 173 | 2 | Q9WD17_EAV | q9wd17 | equine arte |
| 1364 | 72.5 | 6.1 | 174 | 2 | P97065_9ENTR | p97065 | salmonella |
| 1365 | 72.5 | 6.1 | 180 | 2 | P71252_ECOLI | p71252 | escherichia |
| 1366 | 72.5 | 6.1 | 180 | 2 | P71254_ECOLI | p71254 | escherichia |
| 1367 | 72.5 | 6.1 | 180 | 2 | P71255_ECOLI | p71255 | escherichia |
| 1368 | 72.5 | 6.1 | 180 | 2 | P71256_ECOLI | p71256 | escherichia |
| 1369 | 72.5 | 6.1 | 180 | 2 | P71258_ECOLI | p71258 | escherichia |
| 1370 | 72.5 | 6.1 | 180 | 2 | P71259_ECOLI | p71259 | escherichia |
| 1371 | 72.5 | 6.1 | 180 | 2 | P71260_ECOLI | p71260 | escherichia |
| 1372 | 72.5 | 6.1 | 180 | 2 | P71261_ECOLI | p71261 | escherichia |
| 1373 | 72.5 | 6.1 | 183 | 2 | Q55TU2_CRYNE | q55tu2 | cryptococcu |
| 1374 | 72.5 | 6.1 | 191 | 2 | Q8U4P0_PYRFU | q8u4p0 | pyrococcus |
| 1375 | 72.5 | 6.1 | 208 | 2 | Q63447_ECHDI | q63447 | echinotrix |
| 1376 | 72.5 | 6.1 | 208 | 2 | Q7J7L2_ECHDI | q7j7l2 | echinotrix |
| 1377 | 72.5 | 6.1 | 209 | 2 | Q7J7L0_ECHDI | q7j7l0 | echinotrix |
| 1378 | 72.5 | 6.1 | 209 | 2 | Q7J712_ECHDI | q7j712 | echinotrix |
| 1379 | 72.5 | 6.1 | 209 | 2 | Q7J7L3_ECHDI | q7j7l3 | echinotrix |
| 1380 | 72.5 | 6.1 | 210 | 2 | Q7J719_ECHDI | q7j719 | echinotrix |
| 1381 | 72.5 | 6.1 | 211 | 2 | Q9XMK7_OCHPR | q9xmk7 | ochotona pr |
| 1382 | 72.5 | 6.1 | 214 | 2 | O40J90_EHRCH | o40j90 | ehrlichia c |
| 1383 | 72.5 | 6.1 | 217 | 2 | Q31YX9_SHIBS | q31yx9 | shigella bo |
| 1384 | 72.5 | 6.1 | 220 | 2 | Q3YZU8_SHISS | q3yzu8 | shigella so |
| 1385 | 72.5 | 6.1 | 222 | 2 | Q8RGE6_FUSNN | q8rge6 | fusobacteri |
| 1386 | 72.5 | 6.1 | 224 | 2 | Q4MHS9_BACCE | q4mhs9 | bacillus ce |
| 1387 | 72.5 | 6.1 | 243 | 2 | Q7M2C0_LEIMA | q7m2c0 | leishmania |
| 1388 | 72.5 | 6.1 | 255 | 2 | Q3HA88_TRIER | q3ha88 | trichodesmi |
| 1389 | 72.5 | 6.1 | 267 | 2 | Q4S673_TETNG | q4s673 | tetraodon n |
| 1390 | 72.5 | 6.1 | 267 | 2 | Q8RS59_FUSNN | q8rs59 | fusobacteri |
| 1391 | 72.5 | 6.1 | 285 | 2 | Q86DD6_CAEEL | q86dd6 | caenorhabdi |
| 1392 | 72.5 | 6.1 | 288 | 2 | Q2WLM6_CLOBE | q2wlm6 | clostridium |
| 1393 | 72.5 | 6.1 | 291 | 2 | Q24561_BACSK | q24561 | bacillus (m |
| 1394 | 72.5 | 6.1 | 298 | 2 | Q5WL74_BACSK | q5wl74 | bacillus cl |
| 1395 | 72.5 | 6.1 | 298 | 2 | Q8R2A8_MOUSE | q8r2a8 | mus musculu |
| 1396 | 72.5 | 6.1 | 298 | 2 | Q61ZV8_CAEBR | q61zv8 | caenorhabdi |
| 1397 | 72.5 | 6.1 | 307 | 2 | Q6N472_RHOPA | q6n472 | rhodopseudo |
| 1398 | 72.5 | 6.1 | 308 | 2 | Q71UE1_BOVIN | q71ue1 | bos taurus |
| 1399 | 72.5 | 6.1 | 309 | 2 | Q5J2F7_CHIHI | q5j2f7 | chimarrogal |
| 1400 | 72.5 | 6.1 | 310 | 2 | Q5WL95_BACSK | q5wl95 | bacillus cl |
| 1401 | 72.5 | 6.1 | 310 | 2 | Q5WPB4_9DIPT | q5wpb4 | dermatobia |
| 1402 | 72.5 | 6.1 | 315 | 2 | Q9LG02_ARATH | q9lg02 | arabidopsis |
| 1403 | 72.5 | 6.1 | 315 | 2 | Q9CII9_LACLA | q9cii9 | lactococcus |
| 1404 | 72.5 | 6.1 | 320 | 1 | O17077_CAEEL | o17077 | caenorhabdi |
| 1405 | 72.5 | 6.1 | 325 | 2 | Q833B9_ENTFA | q833b9 | enterococcu |
| 1406 | 72.5 | 6.1 | 336 | 2 | Q99924_CYPRI | q99924 | cyprinella |
| 1407 | 72.5 | 6.1 | 348 | 2 | Q83S12_ENTPA | q83s12 | enterococcu |
| 1408 | 72.5 | 6.1 | 348 | 2 | Q5UES6_ECOLI | q5ues6 | escherichia |
| 1409 | 72.5 | 6.1 | 350 | 2 | Q57442_ECOLI | q57442 | escherichia |
| 1410 | 72.5 | 6.1 | 355 | 2 | Q8FXM4_BRUSU | q8fxm4 | brucella su |
| 1411 | 72.5 | 6.1 | 356 | 2 | Q2YIF9_BRUA2 | q2yif9 | brucella ab |
| 1412 | 72.5 | 6.1 | 356 | 2 | O70US3_DIRIM | o70us3 | dirofilaria |
| 1413 | 72.5 | 6.1 | 356 | 2 | Q70US3_DIRIM | q70us3 | dirofilaria |
| 1414 | 72.5 | 6.1 | 360 | 2 | Q6HGU9_BACHK | q6hgu9 | bacillus th |
| 1415 | 72.5 | 6.1 | 363 | 2 | Q4L629_STAHJ | q4l629 | staphylococ |
| 1416 | 72.5 | 6.1 | 365 | 2 | Q8WMR0_SHEEP | q8wmr0 | ovis aries |
| 1417 | 72.5 | 6.1 | 365 | 2 | | | |
| 1418 | 72.5 | 6.1 | 374 | 2 | | | |

| No. | %id | e | Len | N | Entry name | Accession | Description |
|---|---|---|---|---|---|---|---|
| 1419 | 72.5 | 6.1 | 377 | 2 | Q4R215_VARHI | | Q4r215 vargula hil |
| 1420 | 72.5 | 6.1 | 379 | 1 | CYB_CHIHI | Q85av3 | chimarrogal |
| 1421 | 72.5 | 6.1 | 379 | 1 | CYB_OCHAL | Q9gby1 | ochotona al |
| 1422 | 72.5 | 6.1 | 379 | 1 | CYB_OCHCU | Q9g1b9 | ochotona cu |
| 1423 | 72.5 | 6.1 | 379 | 1 | CYB_OCHHI | Q9gby6 | ochotona hi |
| 1424 | 72.5 | 6.1 | 379 | 2 | CYB_OCHHY | Q9g6g2 | ochotona hy |
| 1425 | 72.5 | 6.1 | 379 | 2 | CYB_OCHKO | Q9gbz0 | ochotona ko |
| 1426 | 72.5 | 6.1 | 379 | 1 | CYB_OCHLA | Q9gbz1 | ochotona la |
| 1427 | 72.5 | 6.1 | 379 | 1 | CYB_OCHNB | Q9gbz2 | ochotona nu |
| 1428 | 72.5 | 6.1 | 379 | 1 | CYB_OCHRU | Q9gbz5 | ochotona ro |
| 1429 | 72.5 | 6.1 | 379 | 1 | CYB_OCHTH | Q9gbz6 | ochotona th |
| 1430 | 72.5 | 6.1 | 379 | 1 | CYB_OCHRU | Q9zzu1 | ochotona ru |
| 1431 | 72.5 | 6.1 | 379 | 1 | CYB_OCHTI | | ochotona th |
| 1432 | 72.5 | 6.1 | 379 | 1 | O3LHY6_CHIPT | | ochotona pr |
| 1433 | 72.5 | 6.1 | 379 | 2 | O3LHY7_CHIPT | | chimarrogal |
| 1434 | 72.5 | 6.1 | 379 | 2 | O3LHZ0_CHIPT | | chimarrogal |
| 1435 | 72.5 | 6.1 | 379 | 2 | O3LHZ2_CHIPT | | chimarrogal |
| 1436 | 72.5 | 6.1 | 379 | 2 | O3LHZ7_CHIPT | | chimarrogal |
| 1437 | 72.5 | 6.1 | 379 | 2 | O3LI03_CHIPT | | chimarrogal |
| 1438 | 72.5 | 6.1 | 379 | 2 | O3LI07_CHIPT | | chimarrogal |
| 1439 | 72.5 | 6.1 | 379 | 2 | O3LI15_CHIPT | | chimarrogal |
| 1440 | 72.5 | 6.1 | 379 | 2 | O3LI18_CHIPT | | chimarrogal |
| 1441 | 72.5 | 6.1 | 379 | 2 | O3LI21_CHIPT | | chimarrogal |
| 1442 | 72.5 | 6.1 | 379 | 2 | O3LI32_CHIPT | | chimarrogal |
| 1443 | 72.5 | 6.1 | 379 | 2 | O3LI39_CHIPT | | chimarrogal |
| 1444 | 72.5 | 6.1 | 379 | 2 | O3LI49_CHIPT | | chimarrogal |
| 1445 | 72.5 | 6.1 | 379 | 2 | O7UT5_OCHPR | | chimarrogal |
| 1446 | 72.5 | 6.1 | 379 | 2 | O70UT5_OCHPR | | chimarrogal |
| 1447 | 72.5 | 6.1 | 379 | 2 | O71LX8_9LAGO | | chimarrogal |
| 1448 | 72.5 | 6.1 | 379 | 2 | Q9G1C3_9LAGO | | chimarrogal |
| 1449 | 72.5 | 6.1 | 379 | 2 | Q9G1C4_9LAGO | | chimarrogal |
| 1450 | 72.5 | 6.1 | 379 | 2 | Q9GBY2_9LAGO | | chimarrogal |
| 1451 | 72.5 | 6.1 | 379 | 2 | Q9GBY8_9LAGO | | chimarrogal |
| 1452 | 72.5 | 6.1 | 379 | 2 | Q9GBY9_OCHHY | | ochotona hy |
| 1453 | 72.5 | 6.1 | 379 | 2 | Q9GBZ3_OCHPA | | ochotona pa |
| 1454 | 72.5 | 6.1 | 379 | 2 | O8EWI6_MYCPE | | mycoplasma |
| 1455 | 72.5 | 6.1 | 379 | 2 | Q508J6_PERPA | | perognathus |
| 1456 | 72.5 | 6.1 | 379 | 2 | Q508P1_MICMC | | microdipodo |
| 1457 | 72.5 | 6.1 | 379 | 2 | Q508P2_9RODE | | microdipodo |
| 1458 | 72.5 | 6.1 | 379 | 2 | Q9gaw7_9RODE | | chaetodipus |
| 1459 | 72.5 | 6.1 | 387 | 2 | Q6RKP6_EBVG | | epstein-bar |
| 1460 | 72.5 | 6.1 | 388 | 2 | Q2MDP6_CROCR | | crocuta cro |
| 1461 | 72.5 | 6.1 | 389 | 2 | P30559_HUMAN | | homo sapien |
| 1462 | 72.5 | 6.1 | 395 | 2 | Q32827_SHIDS | | shigella dy |
| 1463 | 72.5 | 6.1 | 402 | 2 | O8WMO9_SHEEP | | ovis aries |
| 1464 | 72.5 | 6.1 | 404 | 2 | Q2SCC2_9GAMM | | habella che |
| 1465 | 72.5 | 6.1 | 428 | 2 | O66CF9_YERPS | | yersinia ps |
| 1466 | 72.5 | 6.1 | 428 | 2 | O8ZG86_YERPE | | yersinia pe |
| 1467 | 72.5 | 6.1 | 435 | 2 | O31E26_THICR | | thiomicrosp |
| 1468 | 72.5 | 6.1 | 442 | 2 | Q6LO Y3_PICTO | | picrophilus |
| 1469 | 72.5 | 6.1 | 442 | 2 | O6PHK5_BRARE | | brachydanio |
| 1470 | 72.5 | 6.1 | 445 | 2 | O6NYH8_BRARE | | brachydanio |
| 1471 | 72.5 | 6.1 | 452 | 2 | Q9I9N6_9BIIA | | terebratuli |
| 1472 | 72.5 | 6.1 | 457 | 2 | O9T9N6_XENTR | | xenopus tro |
| 1473 | 72.5 | 6.1 | 478 | 2 | Q97OD2_SULTO | | sulfolobus |
| 1474 | 72.5 | 6.1 | 488 | 2 | Q4HEC1_CAMCO | | campylobact |
| 1475 | 72.5 | 6.1 | 488 | 2 | Q4HLM0_CAMLA | | campylobact |
| 1476 | 72.5 | 6.1 | 491 | 2 | Q6SWL8_HCMV | | human cytom |
| 1477 | 72.5 | 6.1 | 499 | 1 | MVIN_AQUAE | | aquifex aeo |
| 1478 | 72.5 | 6.1 | 505 | 2 | O8QRV6_9BETA | | pongine her |
| 1479 | 72.5 | 6.1 | 509 | 2 | Q4APJ8_9CHLB | | chlorobium |
| 1480 | 72.5 | 6.1 | 513 | 1 | PACR_BOVIN | | bos taurus |
| 1481 | 72.5 | 6.1 | 521 | 1 | Q2RIT1_MOOTH | | moorella th |
| 1482 | 72.5 | 6.1 | 521 | 2 | Q4QLI3_HAEI8 | | haemophilus |
| 1483 | 72.5 | 6.1 | 522 | 2 | Q23444_CAEEL | | caenorhabdi |
| 1484 | 72.5 | 6.1 | 526 | 2 | Q6FDF6_ACIAD | | acinetobact |
| 1485 | 72.5 | 6.1 | 528 | 2 | Q40LE0_DESAC | | desulfuromo |
| 1486 | 72.5 | 6.1 | 528 | 2 | Q4RQI2_TETNG | | tetraodon n |
| 1487 | 72.5 | 6.1 | 539 | 2 | Q5CU37_CRPEV | | cryptospori |
| 1488 | 72.5 | 6.1 | 539 | 2 | Q7VSL1_BORPE | | bordetella |
| 1489 | 72.5 | 6.1 | 539 | 2 | Q7W446_BORPA | | bordetella |
| 1490 | 72.5 | 6.1 | 539 | 2 | Q7WFK3_BORPA | | bordetella |
| 1491 | 72.5 | 6.1 | 562 | 2 | Q5FIM1_MYTGA | | mytilus gal |

| No. | %id | e | Len | N | Accession | Description |
|---|---|---|---|---|---|---|
| 1492 | 72.5 | 6.1 | 567 | 2 | Q4YTZ9_PLABE | Q4ytz9 plasmodium |
| 1493 | 72.5 | 6.1 | 574 | 2 | Q2X1N5_9GAMM | Q2x1n5 shewanella |
| 1494 | 72.5 | 6.1 | 574 | 2 | Q35VD8_9GAMM | Q35vd8 shewanella |
| 1495 | 72.5 | 6.1 | 574 | 2 | Q6LH28_PHOPR | Q6lh28 photobacter |
| 1496 | 72.5 | 6.1 | 580 | 2 | Q3X6Y0_METFL | Q3x6y0 methylobact |
| 1497 | 72.5 | 6.1 | 614 | 2 | Q34X67_9GAMM | Q34x67 alkalilimni |
| 1498 | 72.5 | 6.1 | 614 | 2 | Q7U5J3_SYNPX | Q7u5j3 synechococc |
| 1499 | 72.5 | 6.1 | 622 | 2 | Q4B546_9BURK | Q4b546 polaromonas |
| 1500 | 72.5 | 6.1 | 635 | 2 | O21335_CAEEL | O21335 caenorhabdi |

ALIGNMENTS

RESULT 1

MENTO_HUMAN

```
ID   MENTO_HUMAN    STANDARD;    PRT;   234 AA.
AC   O95772;
DT   15-NOV-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-MAY-1999, sequence version 1.
DT   07-FEB-2006, entry version 39.
DE   MLN64 N-terminal domain homolog (STARD3 N-terminal-like protein).
DE   Name=STARD3NL; Synonyms=MENTHO; ORFNames=UNQ855/PRO1864;
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, CHARACTERIZATION, TOPOLOGY, PHOSPHORYLATION, AND
RP   ALTERNATIVE INITIATION.
RC   TISSUE=Fetal brain;
RX   MEDLINE=22384343; PubMed=12393907; DOI=10.1074/jbc.M208290200;
RA   Alpy F., Wendling C., Rio M.-C., Tomasetto C.;
RT   "MENTHO, a MLN64 homologue devoid of the START domain.";
RL   J. Biol. Chem. 277:50780-50787(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA   Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA   Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA   Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA   Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA   Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA   Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA   Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA   Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA   Kozlowicz-Reilly A., Leonard S., Rohling T., Rock S.M.,
RA   Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA   Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA   Wendl M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA   Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA   Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA   Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA   Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K.,
RA   Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA   Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
```

**RESULT 1**

```
RA   Bailey J.A., Portnoy M.E., Torrents D., Chiwalla A.T., Gish W.R.,
RA   Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA   Waterston R.H., Wilson R.K.
RT   "The DNA sequence of human chromosome 7.";
RL   Nature 424:157-164(2003).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   TISSUE=Brain, and Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!-  SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
     membrane protein.
-!-  ALTERNATIVE PRODUCTS:
     Event=Alternative initiation;
     Comment=2 isoforms, 1 (shown here) and 2, are produced by
     alternative initiation;
-!-  PTM: Phosphorylated.
-!-  SIMILARITY: Contains 1 MENTAL domain.
```

```
EMBL; AJ492267; CAD37353.1; -; mRNA.
EMBL; AY358645; AAQ89008.1; -; mRNA.
EMBL; AC006033; -; -; Genomic_DNA.
EMBL; BC003074; AAH03074.1; -; mRNA.
EMBL; BC005959; AAH05959.1; -; mRNA.
Ensembl; ENSG00000010270; Homo sapiens.
HGNC; HGNC:19169; STARD3NL.
KW   Alternative initiation; Membrane; Phosphorylation; Transmembrane.
FT   CHAIN        1    234   MLN64 N-terminal domain homolog, isoform
FT                          1.
FT                          /FTId=PRO_000021666.
FT   CHAIN        8    234   MLN64 N-terminal domain homolog, isoform
FT                          2.
FT                          /FTId=PRO_000021667.
FT   INIT_MET     8      8   For isoform 2.
FT   TOPO_DOM     1     53   Cytoplasmic (Potential).
FT   TRANSMEM    54     74   Potential.
FT   TOPO_DOM    75     97   Extracellular (Potential).
FT   TRANSMEM    98    118   Potential.
FT   TOPO_DOM   119    122   Cytoplasmic (Potential).
FT   TRANSMEM   123    143   Potential.
FT   TOPO_DOM   144    150   Extracellular (Potential).
FT   TRANSMEM   151    171   Potential.
FT   TOPO_DOM   172    234   Cytoplasmic (Potential).
FT   DOMAIN      48    218   MENTAL.
SQ   SEQUENCE   234 AA;  26655 MW;  AFB7DAE381983FB0 CRC64;
```

```
Qy    1  MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60

Qy   61  FDLLFVTLLMWIIELNVNGGIENTLEKEVMQYDYSSSYFDIFLLAVFRFKVLIIAYAVCRL  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  FDLLFVTLLMWIIELNVNGGIENTLEKEVMQYDYSSSYFDIFLLAVFRFKVLIIAYAVCRL  120

Qy  121  RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA  180

Qy  181  EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGSERAAEEKQDSEKPLLEL  234
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGSERAAEEKQDSEKPLLEL  234
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```
Query Match      100.0%;  Score 1195;  DB 1;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 3.6e-100;
Matches  234;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60
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**RESULT 2**

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Q5U205_RAT
ID   Q5U205_RAT     PRELIMINARY;  PRT;   235 AA.
AC   Q5U205;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   STARD3 N-terminal like (Predicted).
GN   Name=Stard3nl;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   NIH MGC Project;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
```

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EMBL; BC086352; AAH86352.1; -; mRNA.
Ensembl; ENSRNOG00000012126; Rattus norvegicus.
SQ   SEQUENCE   235 AA;  26719 MW;  6238B671397EA775 CRC64;
```

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Qy    1  MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60

Qy   61  FDLLFVTLLMWIIELNVNGGIENTLEKEVMQYDYSSSYFDIFLLAVFRFKVLIIAYAVCRL  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  FDLLFVTLLMWIIELNVNGGIENTLEKEVMQYDYSSSYFDIFLLAVFRFKVLIIAYAVCRL  120

Qy  121  RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA  180

Qy  181  EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGSERAAEEKQDSEKPLLEL  234
         |||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db  181  EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGSERAAEEKQDSEKPLLEL  234
```

```
Query Match       95.5%;  Score 1141.5;  DB 2;  Length 235;
Best Local Similarity   95.7%;  Pred. No. 2.7e-95;
Matches  225;  Conservative  3;  Mismatches  6;  Indels  1;  Gaps  1;

Qy    1  MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60
```

```
Db
Qy    1 MNHLPEDMENTLTGSQSSHASLRDIHSINPGQLMARIESYEGREKKGISDVRRTFCLFVT  60
Db
Qy   61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVRFKVILLAYAVCRL  120
        ||||||||||||||||||||||||: ||:||||||||||||||||||||||: ||||||
Db   61 FDLLFVTLLWIIELNVNGGIENTLKKEVAHYDYSSYFDIFLLAVRFKVILLGYAVCRL  120
Qy  121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA  180
        |||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db  121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGARGYVLPIISFILAWIETWFLDFKVLPQEA  180
Qy  181 EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGS-EAAEEKQDSEKPLLEL  234
        |||||||||||||||||||||:|||||||||||||||| ||:|||||||||||||
Db  181 EEENRLLIVQDASERAALIPAGLSDGQFYSPPESEAGSSEEEAAEEKQDSEKPLLEL  235
```

RESULT 3
MENTO_MOUSE

```
ID   MENTO_MOUSE             STANDARD;      PRT;   235 AA.
AC   Q9DCI3; Q99J63; Q9D356;
DT   15-NOV-2002, integrated into UniProtKB/Swiss-Prot.
DT   15-NOV-2002, sequence version 2.
DT   07-FEB-2006, entry version 29.
DE   MLN64 N-terminal domain homolog.
GN   Name=Stard3nl; Synonyms=Mentho;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Kidney;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reid J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tonaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC       membrane protein (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Name=1;
CC         IsoId=Q9DCI3-1; Sequence=Displayed;
CC         Name=2;
CC         IsoId=Q9DCI3-2; Sequence=VSP_003909;
CC         Note=No experimental confirmation available;
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!- CAUTION: Ref.1 (BAB31166) sequence differs from that shown due to
CC       a frameshift in position 31.
CC   ---------------------------------------------------------------------------
CC   -!- Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC       Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------------
DR   EMBL; AK002760; BAB22337.1; -; mRNA.
DR   EMBL; AK018331; BAB31166.1; ALT_FRAME; mRNA.
DR   EMBL; BC003334; AAH03334.1; -; mRNA.
DR   Ensembl; ENSMUSG00000003062; Mus musculus.
     MGI; MGI:1923455; Stard3nl.
KW   Alternative splicing; Membrane; Transmembrane.
FT   CHAIN         1    235       MLN64 N-terminal domain homolog.
FT                                /FTId=PRO_000096420.
FT   TOPO_DOM      1     53       Cytoplasmic (Potential).
FT   TRANSMEM     54     74       Potential.
FT   TOPO_DOM     75     97       Extracellular (Potential).
FT   TRANSMEM     98    118       Potential.
FT   TOPO_DOM    119    122       Cytoplasmic (Potential).
FT   TRANSMEM    123    143       Potential.
FT   TOPO_DOM    144    150       Extracellular (Potential).
FT   TRANSMEM    151    171       Potential.
FT   TOPO_DOM    172    235       Cytoplasmic (Potential).
FT   DOMAIN       48    218       MENTAL.
FT   VARSPLIC    218    235       SEEAEEKQESEKPLLEL -> RNSSAFRMGIQKSSQPSGG
FT                                AAGTRARFVPKASSCREGRGPLPMWLQ (in isoform
FT                                2).
FT                                /FTId=VSP_003909.
FT   CONFLICT     32     33       QL -> HS (in Ref. 1; BAB22337).
FT   CONFLICT     52     52       R -> G (in Ref. 2).
SQ   SEQUENCE   235 AA;  26811 MW;  F25172S390CB1503 CRC64;
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```
Qy
Db

Query Match             94.9%;  Score 1134.5;  DB 1;  Length 235;
Best Local Similarity   99.9%;  Pred. No 1.2e-94;
Matches 223;  Conservative 5;  Mismatches 6;  Indels 1;  Gaps 1;

Qy    1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60
        |||||||||| |||||||||||| ||||||| ||||||||||||||||||||||||||||
Db    1 MNHLPEDMENTLTGSQSSHASLRDIHSINPAQLMARIESYEGREKKGISDVRRTFCLFVT  60
```

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RESULT 4
Q3U8Q7 MOUSE

Qy    61  FDLLFVTLLWIIELNVNGGIENTLLEKEVMQYDYSSYSFYFDIFLLAYFRFKVLILAYAVCRL  120
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Db    61  FDLLFVTLLWIIELNVNGGIENTLKKEVIHYDYSSYSFYFDIFLLAVFRFKVLILGYAVCRL   120

Qy   121  RHWWAIALTTAVTSAFLLAKVILSKLFSOQGAFGYVLPIISFILAWIETWFLDFKVLPQEA   180
          |||||||||||||||||||||||||||:||:|||||||||||.||||||||||||||||||
Db   121  RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA   180

Qy   181  EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGS-EEAEEKQDSEKPLLEL        234
          |||||||||||||||||||||||||||||||||||||  |||||:|:|||||||
Db   181  EEENRLLIVQDASERAALIPAGLSDGQFYSPPESEAGSEEEAEEKQESEKPLLEL        235
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ID   Q3U8Q7_MOUSE       PRELIMINARY;    PRT;    235 AA.
AC   Q3U8Q7;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE   clone:I830047P07 product:STARD3 N-terminal like, full insert sequence.
GN   Name=Stard3nl;
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;

RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).

RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=22254683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).

RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).

RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa N.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).

RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C.A., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).

RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
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RX   MEDLINE=20499374; PubMed=11041215?; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNA libraries to
RT   prepare full-length-enriched cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori P., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura A., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.;
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AK152116; BAE30960.1; -; mRNA.
DR   MGI; MGI:1923455; Stard3nl.
SQ   SEQUENCE   235 AA;   26811 MW;   F2517Z5390CB1503 CRC64;

Query Match             94.9%;  Score 1134.5;  DB 2;  Length 235;
Best Local Similarity   94.9%;  Pred: No.1.2e-94;
Matches  223;  Conservative  5;  Mismatches  6;  Indels  1;  Gaps  1;

Qy        1 MNHLPEDMENALTGSQOSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60
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Db        1 MNHLPEHMENTLTGSQOSSHASLRDIHSINPAQLMARIESYEGREKKGISDVRRTFCLFVT  60

Qy       61 FDLLFVTLLMIIELNVNGGIENTLKEKEVMQYDYSSYFDIFLLAVRFRKVLIIAYAVCRL 120
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Db       61 FDLLFVTLLMIIELNVNGGIENTLKKEVIHYDYSSYFDIFLLAVRFKVLIGYAVCRL 120

Qy      121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180

Qy      181 EEENRLLIVQDASERAALIPGGLSDGQFYSPSPESEAGS-EEAEEKQDSEKPLLEL 234
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db      181 EEENRLLIVQDASERAALIPAGLSDGQFYSPPESEAGSEEEAEEKQESEKPLLEL 235

RESULT 5
Q3U852  MOUSE
ID   Q3U852_MOUSE    PRELIMINARY;  PRT;  235 AA.
AC   Q3U852;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE   clone:I830067H03 product:STARD3 N-terminal like, full insert sequence.
GN   Name=Stard3nl;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.

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OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group; and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin C., Schneider C., Semple C., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Shiraki T., Waki K., Kawai J., Nakamura M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
DR EMBL; AK152378; BAE31167.1; -; mRNA.
DR MGI; MGI:1923455; Stard3nl.
SQ SEQUENCE 235 AA; 26777 MW; AD551480C9FCF73D8 CRC64;

RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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CC -----------------------------------------------------------------------

Query Match 94.4%; Score 1128.5; DB 2; Length 235;
Best Local Similarity 94.5%; Pred. No. 4.1e-94;
Matches 222; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

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Qy   1 MNHLPEDMENALTGSQOSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60
         ||||||| ||| || ||||||||| |.|||||| |||||||||||||||||||||||| ||
Db   1 MNHLPEHMENTLTGSQOSSHASIRDIHSINPAQLMARIESYEGREKKGISDVRRTFCLIVT  60

Qy  61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFPLLAVRFRKVLILGYAVCRL 120
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Db  61 FDLLFVTLLWIIELNVNGGIENTLKKEVIHYDYYSSYFDIFLLLAVFRFKVLILGYAVCRL 120

Qy 121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFLLAWIETWFLDFKVLPQEA  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFLLAWIETWFLDFKVLPQEA  180

Qy 181 EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGS-EEAAEEKQDSEKLLEL      234
         ||||||| ||||||||||| |||||||||||||||||| ||| ||| ||| ||||
Db 181 EEENRLLLVQDASERAALIPAGLSDGQFYSPPESEAGSEEEAABEKQESEKPLLEL      235
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RESULT 6
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ID   Q6D138_BRARE    PRELIMINARY;    PRT;    227 AA.
AC   Q6D138;
DT   16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT   16-AUG-2004, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   STARD3 N-terminal like.
GN   Name=stard3nl;
OS   Brachydanio rerio (zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;

RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;

RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,

RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RC   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RC   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayasu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RX   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RC   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;

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CC   see http://www.uniprot.org/terms
CC   -------------------------------------------------------------------
RG   NIH MGC Project;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
SQ   SEQUENCE 227 AA; 24C46AD8FF4985C6 CRC64;
DR   ZFIN; ZDB-GENE-040718-4; stard3nl.
SMR; Q6DFR7; 232-443.
DR   Ensembl; ENSDARG00000045421; -; mRNA.
DR   EMBL; BC075752; AAH75752.1; -; mRNA.
SQ   SEQUENCE 227 AA;  Conservative 31; Mismatches 39; Indels 2; Gaps 2;
Matches 155; Conservative 31; Mismatches 39; Indels 2; Gaps 2;
Best Local Similarity  68.3%; Pred. No. 6.7e-64;
Query Match  66.6%; Score 796; DB 2; Length 227;

Qy      8 MENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLFVT  67
          ||||||||||||||||||||||||||||||||||||:|||||||||||:|:|||||||||
Db      1 MDSQCSSSVGSRANLGSLGNINSTPISARVESYEAGEKKGISDVRRTFCLFVTFDLLFVT  60

Qy     68 LLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAYVACRLRHWWAIA 127
          ||||:|||||||||||||||:||||||||||||||||:||:||||||||
Db     61 LLWIIELNVNGGIOQQLEOEVLKYDYHKSFDIFLLAVFRFAALILAYAVCKLRHWWAIA 120

Qy    128 LTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEAEENRLL 187
          |:|:||:|||||||||||:||||||||||||||||||||||||||||||:|:|||||||
Db    121 ITTAITTGFLIVKVVVSKLLSQGAFGYLLPIISFILAWIETWLLDFKVLPQEAGDEIRYL 180

Qy    188 IVQDASERAALI-PGGLSDGQFYSPPESEAGS--EEAEEKQDSEKPLL 232
          ||||||:|||||||||||||||||||||||||||||||||:||:
Db    181 SVQNRLEHEPLLPPGPLSEGLFYSPPESLADSDEDLDDKHDLEKPIV 227
```

RESULT 7
ID   Q6DFR7_XENTR  PRELIMINARY;  PRT;  448 AA.
AC   Q6DFR7;
DT   16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT   16-AUG-2004, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   START domain containing 3.
GN   Name=stard3-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;

---

RA   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -------------------------------------------------------------------
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   -------------------------------------------------------------------
DR   EMBL; BC076666; AAH76666.1; -; mRNA.
DR   SMR; Q6PF40; 232-443.
DR   Ensembl; ENSXETG00000015141; Xenopus tropicalis.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0005694; P:steroid biosynthesis; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE 448 AA; 2686D07C737D4204 CRC64;
Matches 143; Conservative 29; Mismatches 49; Indels 13; Gaps 4;
Best Local Similarity  61.1%; Pred. No. 7.3e-55;
Query Match  58.6%; Score 700.5; DB 2; Length 448;

Qy      1 MNHLP-----EDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFC 56
          :||||     |||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTKLPGDFQPDLERSLPAIASINSSMSQNHVFSPHSLLPR-----EQRRVISDVRRTFC 54

Qy     57 LFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLLAYA 116
          |||||||||||||||||||||||||:|||||||||||||||||||||||:|:|||||||
Db     55 LFVTFDLLFISLLMIIELNTNDGIEKNLEEELLHYDFKNSFPDIFLLAVFRFSVLILAYA 114

Qy    117 VCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVL 176
          ||||||||||||||:||:||||||||||||||||||||||||||||||||||||||||||
Db    115 IVRLRHWWAIAITTLVTSAFLIAKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLDFKVL 174

Qy    177 PQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSGSEEAEEKQDSEK 229
          ||||||||||||||:||:||||||||||||||||||||||||||||:||
Db    175 TQEAEEERWYMAVQOAAGSHPPLLYNGALSDGQFYSPPESFAGSD--NEFDDDEE 226
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RESULT 8
ID   Q6PF40_XENLA  PRELIMINARY;  PRT;  444 AA.
AC   Q6PF40;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   MGC68989 protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]

DR   EMBL; BC057738; AAH57738.1; -; mRNA.
DR   SMR; Q6PF40; 228-439.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; START.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE 444 AA; 50572 MW; 7BEA97317BF48358 CRC64;

Query Match             58.5%;  Score  698.5;  DB  2;  Length  444;
Best Local Similarity   60.9%;
Matches   140;  Conservative   30;  Mismatches   51;  Indels    9;  Gaps    3;

Qy      1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60
            |:|| ||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db      1 MTKIPGDFQPDLERSLPAIASMSQSHVFSPRSLLPR------EQRRAISDVRRTFCLFVT 54

Qy     61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDILFLLAVFRFKVLILLAYAVCRL 120
           |||||:||||||||||:|:|||:|:|:|||||||||||:|||||||||||||:||||:|
Db     55 FDLLFISLLWIIELNTNGIEKNLEEEILYYDFKNSFFDILFLLAVFRFSVLILAYAIVRL 114

Qy    121 RHWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180
           |||||:||:|||||||:|||:|||||||||||||||:||:|||||||||||||||:|
Db    115 RHWAIAITTLVTSAFLIVKVIQSGLLSKGARGYVLPIVSFVLAWLETWFLDFKVLTQEA 174

Qy    181 EEENRLLIVQDASERAALI-PGGLSDGQFYSPPESAGSEEAEEKQDSEK 229
           |||  |   |||:|  |||:||||||||||||||||||| :|  |:
Db    175 EEERWYIAAQAAATHPSLLYNGALSDGQFYSPPESPAGSD-NEFDDEEE 222

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RESULT 9
Q6GNT3_XENLA
ID   Q6GNT3_XENLA   PRELIMINARY;  PRT;   448 AA.
AC   Q6GNT3;
DT   19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   MGC80895 protein.
GN   Name=MGC80895;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
DR   EMBL; BC073419; AAH73419.1; -; mRNA.
DR   SMR; Q6GNT3; 236-443.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; START.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE 448 AA; 51280 MW; 472FF8E7C3B2F5E4 CRC64;

Query Match             57.2%;  Score  684;  DB  2;  Length  448;
Best Local Similarity   59.7%;
Matches   139;  Conservative   34;  Mismatches   48;  Indels   12;  Gaps    4;

Qy      1 MNHLP----EDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFC 56
            | || | |   |:| | |:|::|:|:|| ::| |  ||||||||||||
Db      1 MTKLPGEFQPDLERSLPAIASINSSMSHHVVSPHSLLPR------EQRRLISDVRRTFC 54

Qy     57 LFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIIFLLAVFRFKVLILLAYA 116
           ||||||||||:||||||||:|||:|:|:|:| ||||:|:|||||||||||:||||:||||
Db     55 LFVTFDLLFISLLWIIELNTNGIEKNLEEEILHYDFKNSFFDILFLLAVFRFSVLILAYA 114

Qy    117 VCRLRHWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVL 176
           :|:|RHWAIA:TT|VTSAFL:|KVI|S||||||||||||:SF:|AW:ETWFLDFKVL
Db    115 IVRLRHWAIAITTLVTSAFLIVKVIQSGLLSKGARGYVLPIVSFVLAWLETWFLDFKVL 174

Qy    177 PQEAEEENRLLIVQ-DASERAALIPGGLSDGQFYSPPESAGSE-EAEEKQDS 227
           :||||||  |    |||  :    | |:|||||||||||:|||| :| |:|
Db    175 TQEAEEERWYIAAQAPANHPPYLYNGTLSDGQFYSPPESPAGSDNEFEDEEEA 227

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RESULT 10
ID   MLN64_HUMAN    STANDARD;    PRT;    445 AA.
AC   Q14849; Q96HM9;
DT   30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 51.
DE   MLN 64 protein (StAR-related lipid transfer protein 3) (StARD3) (START
DE   domain-containing protein 3) (CAB1 protein).
GN   Name=STARD3; Synonyms=CAB1, MLN64;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Mammary carcinoma;
RX   MEDLINE=96039245; PubMed=7490069;
RA   Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
RA   Chenard M.-P., Lidereau R., Basset P., Rio M.-C.;
RT   "Identification of four novel human genes amplified and overexpressed
RT   in breast carcinoma and localized to the q11-q21.3 region of
RT   chromosome 17.";
RL   Genomics 28:367-376(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Oesophageal carcinoma;
RX   MEDLINE=97413641; PubMed=9270027;
RA   Akiyama N., Sasaki H., Ishizuka T., Kishi T., Sakamoto H., Onda M.,
RA   Hirai H., Yazaki Y., Sugimura T., Terada M.;
RT   "Isolation of a candidate gene, CAB1, for cholesterol transport to
RT   mitochondria from the c-ERBB-2 amplicon by a modified cDNA selection
RT   method.";
RL   Cancer Res. 57:3548-3553(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lung, Skin, and Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H.F., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 216-445.
RX   MEDLINE=20264523; PubMed=10802740; DOI=10.1038/75192;
RA   Tsujishita Y., Hurley J.H.;
RT   "Structure and lipid transport mechanism of a StAR-related domain.";
RL   Nat. Struct. Biol. 7:408-414(2000).
RN   [5]
RP   TOPOLOGY.
RX   MEDLINE=21264925; PubMed=11053434; DOI=10.1074/jbc.M00627920200;
RA   Alpy F., Stoeckel M.-E., Dierich A., Escola J.-M., Wendling C.,
RA   Chenard M.-P., Vanier M.T., Gruenberg J., Tomasetto C., Rio M.-C.;
RT   "The steroidogenic acute regulatory protein homolog MLN64, a late
RT   endosomal cholesterol-binding protein.";
RL   J. Biol. Chem. 276:4261-4269(2001).
CC   -!- FUNCTION: Binds and transports cholesterol. Promotes
CC       steroidogenesis in placenta and brain.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC       membrane protein.
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!- SIMILARITY: Contains 1 START domain.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/MLN64ID202.html"
CC   ---------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------------
DR   EMBL; X80198; CAA56489.1; -; mRNA.
DR   EMBL; D38255; BAA22525.1; -; mRNA.
DR   EMBL; BC008356; AAH08356.1; -; mRNA.
DR   EMBL; BC008747; AAH08747.1; -; mRNA.
DR   EMBL; BC025679; AAH25679.1; -; mRNA.
DR   PIR; I38027; I38027.
DR   PDB; 1EM2; X-ray; A=216-444.
DR   Ensembl; ENSG00000131748; Homo sapiens.
DR   H-InvDB; HIX0013780; -.
DR   HGNC; HGNC:17579; STARD3.
DR   MIM; 607048; gene.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0008203; P:cholesterol metabolism; TAS.
DR   GO; GO:0006629; P:lipid metabolism; TAS.
DR   GO; GO:0006839; P:mitochondrial transport; TAS.
DR   GO; GO:0008202; P:steroid metabolism; TAS.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   3D-structure; Lipid transport; Lipid-binding; Membrane;
KW   Steroidogenesis; Transmembrane; Transport.
FT   CHAIN         1    445       MLN 64 protein.
FT                                /FTId=PRO_0000220653.
FT   TOPO_DOM      1     51       Cytoplasmic (Potential).
FT   TRANSMEM     52     72       Potential.
FT   TOPO_DOM     73     94       Extracellular (Potential).
FT   TRANSMEM     95    115       Potential.
FT   TOPO_DOM    116    120       Cytoplasmic (Potential).
FT   TRANSMEM    121    141       Potential.
FT   TOPO_DOM    142    148       Extracellular (Potential).
FT   TRANSMEM    149    169       Potential.
FT   TOPO_DOM    170    445       Cytoplasmic (Potential).
FT   DOMAIN       46    217       MENTAL.
FT   DOMAIN      230    443       START.
FT   CONFLICT    117    117       Q -> R (in Ref. 3; AAH25679).
FT   CONFLICT    216    216       G -> A (in Ref. 3; AAH25679).
FT   HELIX       233    258
FT   STRAND      260    264
FT   TURN        266    267
FT   STRAND      270    276
FT   TURN        277    279
FT   STRAND      280    291
FT   HELIX       293    299
FT   TURN        300    302
FT   HELIX       304    307
FT   TURN        308    310
FT   TURN        312    313
FT   STRAND      314    323
FT   TURN        324    326
FT   STRAND      327    334
FT   TURN        337    337
FT   STRAND      338    341
FT   TURN        342    342
FT   STRAND      345    355
FT   STRAND      357    366
FT   TURN        370    371
FT   STRAND      372    372
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FT   TURN        376    377
FT   STRAND      378    380
FT   STRAND      382    383
FT   STRAND      385    392
FT   STRAND      394    395
FT   TURN        397    398
FT   STRAND      400    406
FT   STRAND      408    409
FT   STRAND      412    414
FT   HELIX       416    440
FT   TURN        441    442
SQ   SEQUENCE    445 AA;   50474 MW;   62BED5C3EDA0DDEF CRC64;
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Query Match           55.6%;   Score 664;  DB 1;  Length 445;
Best Local Similarity 56.2%;   Pred. No. 1.5e-51;
Matches 135;  Conservative  38;  Mismatches 45;  Indels  22;  Gaps   5;

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Qy    1 MNHLP------EDMENAL-----TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
             |:.||     |.|:|          :|| ||||
Db    1 MSKLPRELTRDLERSLPAVASLGSSLSHSQSLSSHLLPPE-------------KRRAISDV 49

Qy  112 ILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL 171
         ||||||||||||||||||||:||:||||:|||||||||:|||||||:|||||:|||||||
Db  110 LLGYAVLQLRHWWVIAVTTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFL 169

Qy   52 RRTFCLFVTFDLLFVTLLWIIELNVVNGGIENTLEKEVMQYDYSSYFDIFLLLAVFRFKVL 111
         |||||||||||||:::|||||||||:|||||||||||:|||:|||||:||:||||||||
Db   50 RRTFCLFVTFDLLFISLLWIIELNTNTGIRKNLEQEIIQYNFKTSFFDIFVLAFFRSGL 109

Qy  172 DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEEKQDSEK 229
         ||||||||||||::||:||||:|||||   ||||||:|||||||||||  :||:||:||
Db  170 DFKVLPQEAEEERWYLAAQVAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVAGKK 229
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RESULT 11
ID   Q53Y53_HUMAN      PRELIMINARY;    PRT;   445 AA.
AC   Q53Y53;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   START domain containing 3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT006964; AAP35610.1; -; mRNA.
DR   SMR; Q53Y53; 230-443.
DR   Ensembl; ENSG00000131748; Homo sapiens.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   GO; GO:0006695; P:cholesterol biosynthesis; IEA.
DR   InterPro; IPR000799; START.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00078; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE   445 AA;   50474 MW;   62BED5C3EDA0DDEF CRC64;

Query Match           55.6%;   Score 664;  DB 2;  Length 445;
Best Local Similarity 56.2%;   Pred. No. 1.5e-51;
Matches 135;  Conservative  38;  Mismatches 45;  Indels  22;  Gaps   5;

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Qy    1 MNHLP------EDMENAL-----TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
             |:.||     |.|:|          :|| ||||
Db    1 MSKLPRELTRDLERSLPAVASLGSSLSHSQSLSSHLLPPE-------------KRRAISDV 49

Qy  112 ILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL 171
         ||||||||||||||||||||:||:||||:|||||||||:|||||||:|||||:|||||||
Db  110 LLGYAVLQLRHWWVIAVTTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFL 169

Qy   52 RRTFCLFVTFDLLFVTLLWIIELNVVNGGIENTLEKEVMQYDYSSYFDIFLLLAVFRFKVL 111
         |||||||||||||:::|||||||||:|||||||||||:|||:|||||:||:||||||||
Db   50 RRTFCLFVTFDLLFISLLWIIELNTNTGIRKNLEQEIIQYNFKTSFFDIFVLAFFRSGL 109

Qy  172 DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEEKQDSEK 229
         ||||||||||||::||:||||:|||||   ||||||:|||||||||||  :||:||:||
Db  170 DFKVLPQEAEEERWYLAAQVAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVAGKK 229
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RESULT 12
ID   MLN64_MOUSE     STANDARD;    PRT;   446 AA.
AC   Q61542;
DT   30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 45.
DE   MLN 64 protein (START-related lipid transfer protein 3) (StARD3)
DE   domain-containing protein 3) (ES 64 protein).
GN   Name=Stard3; Synonyms=Es64, Mln64;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
...
RL   Genomics 28:367-376(1995).

CC   -!- FUNCTION: Binds and transports cholesterol. Promotes
CC       steroidogenesis in placenta and brain (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC       membrane protein (By similarity).

```
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!- SIMILARITY: Contains 1 START domain.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; X82457; CAA57834.1; -; mRNA.
DR   EMBL; BC003313; AAH03313.1; -; mRNA.
DR   HSSP; Q14849; 1EM2.
DR   SMR; Q61542; 231-444.
DR   Ensembl; ENSMUSG00000018167; Mus musculus.
DR   MGI; MGI:1929618; Stard3.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005770; C:late endosome; TAS.
DR   InterPro; IPR000799; C:late endosome; TAS.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   Lipid transport; Lipid-binding; Membrane; Steroidogenesis;
KW   Transmembrane; Transport.
FT   CHAIN         1    446       MLN 64 protein.
FT                                /FTId=PRO_0000220654.
FT   TOPO_DOM      1     52       Cytoplasmic (Potential).
FT   TRANSMEM     53     73       Potential.
FT   TOPO_DOM     74     95       Extracellular (Potential).
FT   TRANSMEM     96    116       Potential.
FT   TOPO_DOM    117    121       Cytoplasmic (Potential).
FT   TRANSMEM    122    142       Potential.
FT   TOPO_DOM    143    149       Extracellular (Potential).
FT   TRANSMEM    150    170       Potential.
FT   TOPO_DOM    171    218       Cytoplasmic (Potential).
FT   DOMAIN       47    218       MENTAL.
FT   DOMAIN      231    444       START.
SQ   SEQUENCE   446 AA;  50470 MW;  DBF435604F3E1E2 CRC64;
```

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Qy        7  DMENAL------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTF   61
                  :|:|:                        :|:|  ||||||||||||||
Db       11  DLERSLPALASLGTSLSHGQSLSSHFIPPL----------EKRAISDVRRTFCLFVTF   60

Qy       62  DLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLR  121
                |:||||||||||||||||||||  |   ||| ||||||||||||||||||||||||
Db       61  DLLFISLLWIIELNTNTGIRKNLEQEVIHYSFQSSFFDIFVLAFFRFSGLLLGYAVLRLQ  120

Qy      122  HWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEAE  181
                ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  HWWVIAVTTLVSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFLDFKVLPQEAE  180

Qy      182  EENRLLIVQDASERAALI-PGGLSDGQOFYSPPEESEAGSE-EAEEKQDSEK  229
                  ||||||||||||||  |||||||||||||||||||  ||||||||||
Db      181  EERWYLAAQAAVARGPLIFSGALSEGQOFYSPPESFAGSDNESDEEVTGKK  230
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RESULT 13
ID      Q544C3_MOUSE  PRELIMINARY;  PRT;  446 AA.
AC      Q544C3;
DT      24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT      24-MAY-2005, sequence version 1.
DT      07-FEB-2006, entry version 9.
DE      3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE      clone:A630020B16 product:steroidogenic acute regulatory protein
DE      related full insert sequence.
DE      cDNA, RIKEN full-length enriched library, clone:F63020P06
DE      product:START domain containing 3, full insert sequence).
GN      Name=Stard3;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; and NOD; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; and NOD; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group; and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; and NOD; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA  Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA  Kanai A., Kawaji H., Kawagawa Y., Kedzierski R.M., King B.L.,
RA  Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA  Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA  Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA  Petrovsky N., Pillai R., Pontius J.U., Qi L., Ramachandran S.,
RA  Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA  Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA  Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA  Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA  Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA  Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA  Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA  Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA  Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA  Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA  Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA  Birney E., Hayashizaki Y.;
RT  "Analysis of the mouse transcriptome based on functional annotation of
RT  60,770 full-length cDNAs.";
RL  Nature 420:563-573(2002).
RN  [5]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J, and NOD; TISSUE=Thymus;
RX  MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA  Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA  Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA  Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA  Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA  Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA  Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA  Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA  Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA  Suzuki H., Toyo-oka T., Wang K.H., Weitz C., Whittaker C.A., Wilming L.,
RA  Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA  Hayashizaki Y.;
RT  "Functional annotation of a full-length mouse cDNA collection.";
RL  Nature 409:685-690(2001).
RN  [6]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J;
RX  MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA  Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA  Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA  Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT  "Normalization and subtraction of cap-trapper-selected cDNAs to
RT  prepare full-length cDNA libraries for rapid discovery of new genes.";
RL  Genome Res. 10:1617-1630(2000).
RN  [7]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J; TISSUE=Thymus;
RA  Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RC  Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RT  "RIKEN integrated sequence analysis (RISA) system-384-format
RT  sequencing integrated pipeline with 384 multicapillary sequencer.";
RL  Genome Res. 10:1757-1771(2000).
RN  [8]

RA  Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA  Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA  Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA  Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA  Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA  Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA  Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA  Tagawa A., Takahashi F., Takahashi T., Takeda Y., Tanaka T.,
RA  Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL  Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN  [9]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=NOD;
RA  Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA  Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA  Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA  Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA  Shibata K., Shiraki T., Tagami M., Tagami Y., Tagami Y., Waki K., Watahiki A.,
RA  Muramatsu M., Hayashizaki Y.;
RL  Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

DR  EMBL; AK041538; BAC30977.1; -; mRNA.
DR  EMBL; AK155124; BAE33063.1; -; mRNA.
SMR; Q54C3; 231-444.
DR  Ensembl; ENSMUSG00000018167; Mus musculus.
DR  MGI; MGI:1929618; Stard3.
DR  GO; GO:0016021; C:integral to membrane; RCA.
DR  GO; GO:0005770; C:late endosome; TAS.
DR  InterPro; IPR000799; StAR.
DR  InterPro; IPR002913; START_lipid_bd.
DR  Pfam; PF01852; START; 1.
DR  PRINTS; PR00978; STARPROTEIN.
DR  SMART; SM00234; START; 1.
DR  PROSITE; PS50848; START; 1.
SQ  SEQUENCE  446 AA;  50470 MW;  DBF435604F3E1E2 CRC64;

Query Match        54.9%;   Score 656.5;  DB 2;   Length 446;
Best Local Similarity  57.8%;   Pred. No. 7.3e-51;
Matches 133;   Conservative 33;   Mismatches 47;   Indels 17;   Gaps 4;

```
Qy         7 DMENAL------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTF 61
             |:|.||      |:|::||| :|| :|  | |||| ||:|:|| || :|||||||||||||
Db        11 DIERSLPALASLGISLSHSQSLSSHFIPPL------------EKRRAISDVRRTFCLFVTF 60

Qy        62 DLLFVTLIWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVRFKVLILAYAVCRLR 121
             |||||:|||||:|||||:||.|  || :|: ||||||||||:|||||:|||||:||||
Db        61 DLLFISLLIWIIELNTNTGIRKNLEQEVIHYSFQSSFFDIFVLAFPRFSGLLLGYAVLRLQ 120

Qy       122 HWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILLAWIETWFLDFKVLPQEAE 181
             ||| :| ||||:|||| |||:|||||||:| || ||| |:|:||| ||:|||||||||||
Db       121 HWWVIAVTLVSSAFLIVKVILSELSKGAFGYLLPIVSFVLAWLETWFDFKVLPQEAE 180

Qy       182 EENRLLIVQDASERAALI-PGGLSDGQFYSPPESRAGSE-EAEEKQDSEK 229
             |:||||||||:|||:||| |||||||||:|||| ||:|| :|||||:|: :|
Db       181 EERWTLAAQAAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVTGKK 230
```

RESULT 15

ID   MLN64_BRARE             STANDARD;      PRT;   448 AA.
AC   Q9DFS4; Q6PH03;

DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-2005, sequence version 2.
DT   07-FEB-2006, entry version 21.
DE   MLN64-like protein (START domain-containing protein 3).
GN   Name=stard3; Synonyms=mln64;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=AB;
RG   NIH - Zebrafish Gene Collection (ZGC) project;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 210-448.
RX   PubMed=11064158; DOI=10.1016/S0303-7207(00)00316-6;
RA   Bauer M.P., Bridgham J.T., Langenau D.M., Johnson A.L., Goetz F.W.;
RT   "Conservation of steroidogenic acute regulatory (StAR) protein
RT   structure and expression in vertebrates.";
RL   Mol. Cell. Endocrinol. 168:119-125(2000).
CC   -!- FUNCTION: Binds and transports cholesterol. Promotes
CC       steroidogenesis (By similarity).
CC   -!- SIMILARITY: Contains 1 START domain.
CC   --------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   --------------------------------------------------------------------------
DR   EMBL; BC056766; AAH56766.1; -; mRNA.
DR   EMBL; AF258786; AAG28603.1; -; mRNA.
DR   HSSP; Q14849; 1EM2.
DR   SMR; Q9DFS4; 232-443.
DR   Ensembl; ENSDARG00000017809; Danio rerio.
DR   ZFIN; ZDB-GENE-001120-2; stard3.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   Lipid transport; Lipid-binding; Steroidogenesis; Transport.
FT   DOMAIN      232    445       START.
FT   CONFLICT    210    220       YSPPESLAGSE -> PGRPRVRPVR (in Ref. 2).
SQ   SEQUENCE   448 AA;  50751 MW;  716A18C127B59C5D CRC64;

Query Match             52.9%;  Score 632;  DB 1;  Length 448;
Best Local Similarity   70.9%;  Pred. No. 1.2e-48;
Matches  127;  Conservative   18;  Mismatches   32;  Indels    2;  Gaps    2;

Qy      44 EKRGISDVRRTFCLFVTFDLLFVTLLWIIELNVVNGGIENTLEKEVMQYDYSSYFDIFLL 103
           |:|||||||||||||||||| |||||||||||||||||||||:||::||::|||||||||
Db      43 ERKAFSDVRRTFCLFVTFDLLFITLLWIIELNISKSIWNSLENEVHVNFKSSFFDIFLL 102

Qy     104 AVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFTL 163
           ||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||:||
Db     103 AVFRFLCLQLGVAAFRLRHWWVIAITLVTTAFLIAKVILSDLFSQNAFGYVLPITSFVV 162

Qy     164 AWIETWFLDFKVLPQEAEEEN-RLLIVQDASERAALI-PGGLSDGQFYSPPESBAGSEE 220
           ||||||||||||||:||||||:|||||||||||||||:|||||||||||||||||||||
Db     163 AWLETWFLDFKVLTQERAEDERVYLAAVNAACPPAPLICPRPVVSDGQFYSPPESLAGSED 221

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RP   [1]
RN   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smailus D.E.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Heart;
RG   NIH MGC Project;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC   --------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   --------------------------------------------------------------------------
DR   EMBL; BC085872; AAH85872.1; -; mRNA.
DR   SMR; Q5U2T5; 231-444.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   446 AA;  50386 MW;  19BF58B56F09722F CRC64;

Query Match             54.9%;  Score 656.5;  DB 2;  Length 446;
Best Local Similarity   56.2%;  Pred. No. 7.3e-51;
Matches  135;  Conservative   32;  Mismatches   52;  Indels   21;  Gaps    4;

Qy       1 MNHLPEDMEN----------ALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
           |:|||||||             ||||||||:||||  ||:||| |:
Db       1 MSKLPGDLAGDLERSLPALASLGTSLSHSQSLSSHFIPPPLEKRRV----------VSDV 50

Qy      52 RRTFCLFVTFDLLFVTLLWIIELNVVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVL 111
           ||||:|||||||||||||||||||:|:||||:::||::||::|||||||||:::
Db      51 RRTFCLFVTFDLLFISLLWIIELNTNGIRKNLEQEVIHYSFQSSFFDIFVLAFFRFSGL 110

Qy     112 IIAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL 171
           ||:||||||||||||||||||||:|| |||||:||||||||||||||:||||||||||||
Db     111 LLGYAVLRLQHWWVIAITLVSSAFLIVKVIISELSKGAFGYVLLPIISFVLAWLETWFL 170

Qy     172 DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESPESEAGSSE-EAEEKQDSEK 229
           ||||||||||||:|||||||||||||||:|||||||||||||||||||||||  |||::||:||
Db     171 DFKVLPQEAEEERWYLAAQAAVARGPLLFSGALSEGQFYSPPESFAGSDSESESDEEVAGKK 230